NewSTEPs
A Program of the Association of Public Health Laboratories™

Case Worksheets for Newborn Screening

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Case Information Worksheet

Question:	Answer
INFANT DEMOGRAPHICS	
State Unique ID? (alphanumeric)	
Date of Birth? (mm/dd/yyyy)	
Gestational Age? (in weeks)	
Birth Weight? (in grams)	
Biological Sex?	☐ Male ☐ Female ☐ Unspecified ☐ Unknown
Race? **(select all that apply)**	☐ White ☐ Black or African American ☐ American Indian or Alaskan Native ☐ Asian ☐ Native Hawaiian or other Pacific Islander ☐ Not Reported/Unknown
Ethnicity? **(select one)**	☐ Hispanic, Latino(a) or Spanish origin ☐ Not of Hispanic, Latino(a), or Spanish origin ☐ Not Reported/Unknown
SCREENING INFORMATION	
Was prenatal testing done that indicated that this infant was at risk for this disorder?	☐ Yes ☐ No ☐ Don't Know
Which newborn screen result indicated this infant was at risk for the disorder?	☐ Initial Screen ☐ 2nd Required Screen ☐ Subsequent Screen
Was this individual diagnosed later in life (not identified by newborn screening)?	☐ Yes ☐ No ☐ Unknown
Date of <u>initial</u> specimen collection (mm/dd/yyyy)?	
Date of receipt by lab of <u>initial</u> specimen (mm/dd/yyyy)?	
Date of release of out of range results of <u>initial</u> specimen (mm/dd/yyyy)?	
Date of <u>subsequent</u> specimen collection (mm/dd/yyyy)?	
Date of receipt by lab of <u>subsequent</u> specimen (mm/dd/yyyy)?	
Date of release of out of range results of <u>subsequent</u> specimen (mm/dd/yyyy)?	
Date of intervention by appropriate medical provider (mm/dd/yyyy)?	
Date of confirmation of diagnosis (mm/dd/yyyy)?	

Newborn Screening Surveillance Case Definitions

Developed by the Health Resources and Services Administration (HRSA) and NewSTEPs in cooperation with the newborn screening medical sub-specialty community, standard surveillance case definitions for newborn screening conditions allow for determination of true prevalence and incidence of disorders, and for comparison of outcomes across states. The case definition forms can be found in the pages to follow, stratified by disorder type. Additionally you can find case definition classification tables [linked here]() that can used as a reference resource.

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Note: standard surveillance case definitions have not been developed for 3-Hydroxy-3-methylglutaric aciduria (HMG) or for ß-Ketothiolase deficiency (ßKT). These are forthcoming.

Metabolic Disorders

Organic Acid Disorders:

Glutaric Acidemia/ Aciduria Type I (GA1)

Case Confirmatory Diagnosis Follow-Up

Instructions: Please answer the questions as fully as possible. All testing refers to confirmatory testing following newborn screening. You may need to consult with relevant clinician(s) and/or medical staff to obtain this information.

Please answer the following as Yes/No/Don't Know	If Yes
Were urine organic acids tested? ☐ Yes ☐ No ☐ Don't Know	Was 3-OH Glutaric acid level ☐ Elevated ☐ Normal ☐ Unknown Was Glutaric acid level ☐ Elevated ☐ Normal ☐ Unknown
Were serum organic acids tested? ☐ Yes ☐ No ☐ Don't Know	Was 3-OH Glutaric acid level ☐ Elevated ☐ Normal ☐ Unknown Was Glutaric acid level ☐ Elevated ☐ Normal ☐ Unknown
Were plasma acylcarnitines tested? ☐ Yes ☐ No ☐ Don't Know	Was C5 -DC level ☐ Elevated ☐ Normal ☐ Unknown
Was a mutation analysis performed for Glutaric aciduria type I? ☐ Yes ☐ No ☐ Don't Know	What genes were included in the mutation analysis? ☐ GCDH gene ☐ Other gene:________________

MOLECULAR GENETICS REPORT	
Were variants detected in the GCDH gene? ☐ Yes ☐ No ☐ Don’t Know	Check the types of variants found on: *Allele 1:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown *Allele 2:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown
Were variants detected in other genes? ☐ Yes ☐ No ☐ Don’t Know	Check the types of variants found on: *Allele 1:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown *Allele 2:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown
Was enzyme analysis for Glutaric Acidemia enzyme activity completed? ☐ Yes ☐ No ☐ Don’t Know	Was enzyme activity: ☐ Consistent with disease ☐ Normal activity (not consistent with disease) ☐ Unknown

Isovaleric Acidemia/ Aciduria (IVA)

Case Confirmatory Diagnosis Follow-Up

Instructions: Please answer the questions as fully as possible. All testing refers to confirmatory testing following newborn screening. You may need to consult with relevant clinician(s) and/or medical staff to obtain this information.

Please answer the following as Yes/No/Don't Know	If Yes
Were urine organic acids tested? ☐ Yes ☐ No ☐ Don't Know	Was 3OH Isovaleric acid level ☐ Elevated ☐ Normal ☐ Unknown Was Isovaleryl glycine level ☐ Elevated ☐ Normal ☐ Unknown
Were plasma acylcarnitines tested? ☐ Yes ☐ No ☐ Don't Know	Was C5 level ☐ Elevated ☐ Normal ☐ Unknown
Was a mutation analysis performed for Isovaleric aciduria? ☐ Yes ☐ No ☐ Don't Know	What genes were included in the mutation analysis? ☐ IVD gene ☐ Other gene:_______________

MOLECULAR GENETICS REPORT

Were variants detected in the IVD gene? ☐ Yes ☐ No ☐ Don’t Know	Check the types of variants found on: *Allele 1:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown *Allele 2:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown
Were variants detected in other genes? ☐ Yes ☐ No ☐ Don’t Know	Check the types of variants found on: *Allele 1:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown *Allele 2:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown
Was enzyme analysis for isovaleric acidemia enzyme activity completed? ☐ Yes ☐ No ☐ Don’t Know	Was enzyme activity: ☐ Consistent with disease ☐ Normal activity (not consistent with disease) ☐ Unknown

3-Methylcrotonyl-CoA Carboxylase Deficiency (3-MCC)

Case Confirmatory Diagnosis Follow-Up

Instructions: Please answer the questions as fully as possible. All testing refers to confirmatory testing following newborn screening. You may need to consult with relevant clinician(s) and/or medical staff to obtain this information.

Please answer the following as Yes/No/Don't Know	If Yes
Were urine organic acids tested? ☐ Yes ☐ No ☐ Don't Know	Was 3OH Isovaleric acid level ☐ Elevated ☐ Normal ☐ Unknown Was 3-methylcrotonyl glycine level ☐ Elevated ☐ Normal ☐ Unknown
Were plasma acylcarnitines tested? ☐ Yes ☐ No ☐ Don't Know	Was C5-OH level ☐ Elevated ☐ Normal ☐ Unknown
Was maternal 3-MCC level tested and ruled out? ☐ Yes ☐ No ☐ Don't Know	[redacted]
Was a mutation analysis performed for 3-MCC? ☐ Yes ☐ No ☐ Don't Know	What genes were included in the mutation analysis? ☐ MCCC1 gene ☐ MCCC2 gene ☐ Other gene: ________________

Molecular Genetics Report

Were variants detected in the MCCC1 gene? ☐ Yes ☐ No ☐ Don't Know	Check the types of variants found on: *Allele 1:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown *Allele 2:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown
Were variants detected in the MCCC2 gene? ☐ Yes ☐ No ☐ Don't Know	Check the types of variants found on: *Allele 1:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown *Allele 2:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown
Were variants detected in other genes? ☐ Yes ☐ No ☐ Don't Know	Check the types of variants found on: *Allele 1:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown *Allele 2:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown
Was enzyme analysis for 3-MCC enzyme activity completed? ☐ Yes ☐ No ☐ Don't Know	Was enzyme activity: ☐ Consistent with disease ☐ Normal activity (not consistent with disease) ☐ Unknown

MMA With Homocystinuria; (CblC; CblD; CblF; CblDv1; CblJ)
Case Confirmatory Diagnosis Follow-Up

Instructions: Please answer the questions as fully as possible. All testing refers to confirmatory testing following newborn screening. You may need to consult with relevant clinician(s) and/or medical staff to obtain this information.

Part I: Final Diagnosis as determined by metabolic geneticist or clinician performing the follow-up

Please Select One:

A. Cobalamin C deficiency (CblC)
B. Cobalamin D deficiency (CblD)
C. Cobalamin F deficiency (CblF)
D. Cobalamin Dv1 deficiency (CblDv1)
E. Cobalamin J deficiency (CblJ)
F. Other cobalamin deficiency not listed above: ______________________________

Please answer the following as Yes/No/Don't Know	If Yes
Was serum MMA level tested? ☐ Yes ☐ No ☐ Don't Know	Was MMA level in serum: ☐ Elevated ☐ Normal ☐ Unknown
Was urine MMA level tested? ☐ Yes ☐ No ☐ Don't Know	Was MMA level in urine: ☐ Elevated ☐ Normal ☐ Unknown
Were plasma acylcarnitines tested? ☐ Yes ☐ No ☐ Don't Know	Was C3: ☐ Elevated ☐ Normal ☐ Unknown
Was maternal vitamin B12 levels tested? ☐ Yes ☐ No ☐ Don't Know	Was maternal vitamin B12 deficient? ☐ Yes ☐ No ☐ Unknown

Were infant vitamin B12 levels tested? ☐ Yes ☐ No ☐ Don’t Know	Was infant vitamin B12 deficient? ☐ Yes ☐ No ☐ Unknown
Was total plasma homocysteine tested? ☐ Yes ☐ No ☐ Don’t Know	Was total plasma homocysteine: ☐ Elevated ☐ Normal ☐ Unknown
Was mutation analysis done? ☐ Yes ☐ No ☐ Don’t Know	What genes were included in the mutation analysis? ☐ C2ORF25 gene (cblD) ☐ MMACHC gene ☐ LMBRD1 gene (cblF) ☐ ABCD4 gene (cblJ) ☐ Other MMA associated gene:__________

MOLECULAR GENETICS REPORT

Were variants found in C2ORF25 gene? ☐ Yes ☐ No ☐ Don’t Know	Check the types of variants found on: *Allele 1:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown *Allele 2:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown
Were variants found in MMACHC gene? ☐ Yes ☐ No ☐ Don’t Know	Check the types of variants found on: *Allele 1:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown *Allele 2:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown

Were variants found in LMBRD1 gene? ☐ Yes ☐ No ☐ Don't Know	Check the types of variants found on: *Allele 1:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown *Allele 2:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown
Were variants found in ABCD4 gene? ☐ Yes ☐ No ☐ Don't Know	Check the types of variants found on: *Allele 1:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown *Allele 2:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown
Were variants found in other MMA related genes?______________ ☐ Yes ☐ No ☐ Don't Know	Check the types of variants found on: *Allele 1:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown *Allele 2:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown
Were enzyme complementation studies completed? ☐ Yes ☐ No ☐ Don't Know	Were complementation studies: ☐ Consistent with disease ☐ Normal activity (not consistent with disease) ☐ Unknown

MMA Without Homocystinuria; (CblA; CblB; mut-; mut0; CblDv2)

Case Confirmatory Diagnosis Follow-Up

Instructions: Please answer the questions as fully as possible. All testing refers to confirmatory testing following newborn screening. You may need to consult with relevant clinician(s) and/or medical staff to obtain this information.

Part I: Final Diagnosis as determined by metabolic geneticist or clinician performing the follow-up

Please Select One:

G. Cobalamin A deficiency (CblA)
H. Cobalamin B deficiency (CblB)
I. Mutase (-) (mut-0)
J. Mutase (0) (mut0)
K. Cobalamin Dv2 (CblDv2)

Please answer the following as Yes/No/Don't Know	If Yes
Was serum MMA level tested? ☐ Yes ☐ No ☐ Don't Know	Was MMA level in serum: ☐ Elevated ☐ Normal ☐ Unknown
Was urine MMA level tested? ☐ Yes ☐ No ☐ Don't Know	Was MMA level in urine: ☐ Elevated ☐ Normal ☐ Unknown
Were plasma acylcarnitines tested? ☐ Yes ☐ No ☐ Don't Know	Was C3: ☐ Elevated ☐ Normal ☐ Unknown
Was maternal vitamin B12 levels tested? ☐ Yes ☐ No ☐ Don't Know	Was maternal vitamin B12 deficient? ☐ Yes ☐ No ☐ Unknown

Were infant vitamin B12 levels tested? ☐ Yes ☐ No ☐ Don't Know	Was infant vitamin B12 deficient? ☐ Yes ☐ No ☐ Unknown
Was total plasma homocysteine tested? ☐ Yes ☐ No ☐ Don't Know	Was total plasma homocysteine: ☐ Elevated ☐ Normal ☐ Unknown
Was mutation analysis done? ☐ Yes ☐ No ☐ Don't Know	What genes were included in the mutation analysis? ☐ METHYLMALONYL-CoA MUTASE ☐ MMAA gene ☐ MMAB gene ☐ Other MMA associated gene:__________
Molecular Genetics Report	
Were variants found in the METHYLMALONYL-CoA MUTASE gene? ☐ Yes ☐ No ☐ Don't Know	Check the types of variants found on: *Allele 1:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown *Allele 2:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown
Were variants found in MMAA gene? ☐ Yes ☐ No ☐ Don't Know	Check the types of variants found on: *Allele 1:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown *Allele 2:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown

Were variants found in MMAB gene? ☐ Yes ☐ No ☐ Don’t Know	Check the types of variants found on: *Allele 1:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown *Allele 2:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown
Were variants found in other MMA related genes?______________ ☐ Yes ☐ No ☐ Don’t Know	Check the types of variants found on: *Allele 1:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown *Allele 2:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown
Were enzyme complementation studies completed? ☐ Yes ☐ No ☐ Don’t Know	Were complementation studies: ☐ Consistent with disease ☐ Normal activity (not consistent with disease) ☐ Unknown

Propionic Acidemia/ Aciduria
Case Confirmatory Diagnosis Follow-Up

Instructions: Please answer the questions as fully as possible. All testing refers to confirmatory testing following newborn screening. You may need to consult with relevant clinician(s) and/or medical staff to obtain this information.

Please answer the following as Yes/No/Don't Know	If Yes
Were urine organic acids tested? ☐ Yes ☐ No ☐ Don't Know	Please indicate which of the following metabolites were detected: Propionyl glycine: ☐ Yes ☐ No ☐ Unknown Tiglyglycine: ☐ Yes ☐ No ☐ Unknown Methylcitrate: ☐ Yes ☐ No ☐ Unknown 3OH propionic acid: ☐ Yes ☐ No ☐ Unknown MMA: ☐ Yes ☐ No ☐ Unknown Methylcrotonyl glycine: ☐ Yes ☐ No ☐ Unknown
Were plasma acylcarnitines tested? ☐ Yes ☐ No ☐ Don't Know	Was C3 level ☐ Elevated ☐ Normal ☐ Unknown

Was a mutation analysis performed for Propionyl-CoA carboxylase (PCC)? ☐ Yes ☐ No ☐ Don't Know	What genes were included in the mutation analysis? ☐ PCCA ☐ PCCB ☐ Other gene:____________
MOLECULAR GENETICS REPORT	
Were variants detected in the PCCA gene? ☐ Yes ☐ No ☐ Don't Know	Check the types of variants found on: *Allele 1:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown *Allele 2:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown
Were variants detected in the PCCB gene? ☐ Yes ☐ No ☐ Don't Know	Check the types of variants found on: *Allele 1:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown *Allele 2:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown

Were variants detected in other genes? ☐ Yes ☐ No ☐ Don't Know	Check the types of variants found on: *Allele 1:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown *Allele 2:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown

Holocarboxylase Synthetase (Multiple Carboxylase) Deficiency or Other Biotin Disorders (Not Biotinidase Deficiency) (MCD)

Case Confirmatory Diagnosis Follow-Up

Instructions: Please answer the question as fully as possible. All testing refers to confirmatory testing following newborn screening. You may need to consult with relevant clinician(s) and/or medical staff to obtain this information.

Final diagnosis as determined by the metabolic geneticist or clinician performing the follow-up:

Please choose one:

A. Holocarboxylase deficiency
B. Other biotin disorder (not biotinidase deficiency)______________________

Please answer the following as Yes/No/Don't Know	If Yes
Were urine organic acids tested? ☐ Yes ☐ No ☐ Don't Know	Was 3OH Isovaleric acid level ☐ Elevated ☐ Normal ☐ Unknown Was 3OH Propionic acid level ☐ Elevated ☐ Normal ☐ Unknown Was 3-methylcrotonyl glycine level ☐ Elevated ☐ Normal ☐ Unknown
Were plasma acylcarnitines tested? ☐ Yes ☐ No ☐ Don't Know	Was C3 level ☐ Elevated ☐ Normal ☐ Unknown Was C5-OH level ☐ Elevated ☐ Normal ☐ Unknown
Were infant chemistries (biotinidase) studies completed? ☐ Yes ☐ No ☐ Don't Know	What were the Biotinadase results? ☐ Normal ☐ Abnormal ☐ Untested/Unknown

Was a mutation analysis performed for Holocarboxylase Synthetase Deficiency? ☐ Yes ☐ No ☐ Don’t Know	What genes were included in the mutation analysis? ☐ HLCS gene ☐ Other gene:_______________

MOLECULAR GENETICS REPORT

Were variants detected in the HLCS gene? ☐ Yes ☐ No ☐ Don’t Know	Check the types of variants found on: *Allele 1:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown *Allele 2:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown
Were variants detected in other genes? ☐ Yes ☐ No ☐ Don’t Know	Check the types of variants found on: *Allele 1:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown *Allele 2:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown
Was enzyme analysis for holocarboxylase synthetase deficiency enzyme activity completed? ☐ Yes ☐ No ☐ Don’t Know	Was enzyme activity: ☐ Consistent with disease ☐ Normal activity (not consistent with disease) ☐ Unknown

Fatty Acid Disorders:

Primary Carnitine Deficiency/ Carnitine Uptake Deficiency (CUD)

Case Confirmatory Diagnosis Follow-Up

Instructions: Please answer the questions as fully as possible. All testing refers to confirmatory testing following newborn screening. You may need to consult with relevant clinician(s) and/or medical staff to obtain this information.

Please answer the following as Yes/No/Don't Know	If Yes
Was urine carnitine tested? ☐ Yes ☐ No ☐ Don't Know	Was fractional excretion of free carnitine level: ☐ Elevated ☐ Normal ☐ Unknown
Were plasma carnitine levels tested? ☐ Yes ☐ No ☐ Don't Know	Was free carnitine (C0) ☐ Low ☐ Normal ☐ Unknown
Were other causes for carnitine loss ruled out? ☐ Yes ☐ No ☐ Don't Know	[redacted]
Was a mutation analysis performed for carnitine transporter defects? ☐ Yes ☐ No ☐ Don't Know	What genes were included in the mutation analysis? ☐ SLC22A5 gene ☐ Other gene:_______________
MOLECULAR GENETICS REPORT	
Were variants detected in the SLC22A5 gene? ☐ Yes ☐ No ☐ Don't Know	Check the types of variants found on: *Allele 1:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown *Allele 2:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown

Were variants detected in other genes? ☐ Yes ☐ No ☐ Don’t Know	Check the types of variants found on: *Allele 1:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown *Allele 2:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown
Was enzyme analysis for carnitine deficiency enzyme activity completed? ☐ Yes ☐ No ☐ Don’t Know	Was enzyme activity: ☐ Consistent with disease ☐ Normal activity (not consistent with disease) ☐ Unknown

Medium-chain acyl-CoA Dehydrogenase Deficiency (MCAD)

Case Confirmatory Diagnosis Follow-Up

Instructions: Please answer the questions as fully as possible. All testing refers to confirmatory testing following newborn screening. You may need to consult with relevant clinician(s) and/or medical staff to obtain this information.

Please answer the following as Yes/No/Don't Know	If Yes
Were urine organic acids or aclyglycines tested? ☐ Yes ☐ No ☐ Don't Know	Was Hexanoylglycine level ☐ Elevated ☐ Normal ☐ Unknown
Were plasma acylcarnitines tested? ☐ Yes ☐ No ☐ Don't Know	Was C8 level: ☐ Elevated ☐ Elevated on repeat testing ☐ Normal ☐ Unknown Was C8>C10 level ☐ Elevated ☐ Normal ☐ Unknown Was C8>C6 level ☐ Elevated ☐ Normal ☐ Unknown Was C6 level ☐ Elevated ☐ Normal ☐ Unknown Was C10 level ☐ Elevated ☐ Normal ☐ Unknown
Was mutation analysis performed for MCAD? ☐ Yes ☐ No ☐ Don't Know	What genes were included in the mutation analysis? ☐ ACADM ☐ Other: ________________

MOLECULARGENETICS REPORT	
Were variants detected in the ACADM gene? ☐ Yes ☐ No ☐ Don’t Know	Check the types of variants found on: *Allele 1:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown *Allele 2:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown
Were variants detected in other genes? ☐ Yes ☐ No ☐ Don’t Know	Check the types of variants found on: *Allele 1:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown *Allele 2:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown
Was functional analysis of fatty acid oxidation in cultured fibroblasts performed? ☐ Yes ☐ No ☐ Don’t Know	Was functional fibroblast analysis: ☐ Consistent with disease ☐ Normal activity (not consistent with disease) ☐ Unknown
Was enzyme analysis for MCAD enzyme activity completed? ☐ Yes ☐ No ☐ Don’t Know	Was enzyme analysis: ☐ Consistent with disease ☐ Normal activity (not consistent with disease) ☐ Unknown

Tri-Functional Protein Deficiency (TFP); Inclusive of LCHAD
Case Confirmatory Diagnosis Follow-Up

Instructions: Please answer the questions as fully as possible. All testing refers to confirmatory testing following newborn screening. You may need to consult with relevant clinician(s) and/or medical staff to obtain this information.

Part I: Final Diagnosis as determined by metabolic geneticist or clinician performing the follow-up

Please select one:

L. Trifunctional Protein Deficiency
M. Long Chain Acyl CoA dehydrogenase deficiency (LCHAD)

Please answer the following as Yes/No/Don't Know	If Yes
Were urine organic acids tested? ☐ Yes ☐ No ☐ Don't Know	Was C12-OH dicarboxylic acid level ☐ Elevated ☐ Normal ☐ Unknown Was C10-OH dicarboxylic level? ☐ Elevated ☐ Normal ☐ Unknown
Were plasma acylcarnitines tested? ☐ Yes ☐ No ☐ Don't Know	Was C16-OH level ☐ Elevated (on more than one sample) ☐ Normal ☐ Unknown Was C16:1-OH level ☐ Elevated ☐ Normal ☐ Unknown Was C18-OH level ☐ Elevated ☐ Normal ☐ Unknown Was C18:1-OH level ☐ Elevated ☐ Normal ☐ Unknown

Was mutation analysis performed for Trifunctional Protein deficiency? ☐ Yes ☐ No ☐ Don't Know	What genes were included in the mutation analysis? ☐ HADHA ☐ HADHB ☐ Other: ________________
Molecular Genetics Report	
Were variants detected in HADHB gene? ☐ Yes ☐ No ☐ Don't Know	Check the types of variants found on: *Allele 1:* ☐ Variant known to be disease causing ☐ Variant of unknown significance ☐ Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown *Allele 2:* ☐ Variant known to be disease causing ☐ Variant of unknown significance ☐ Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown
Were variants detected in HADHA gene? ☐ Yes ☐ No ☐ Don't Know	Check the types of variants found on: *Allele 1:* ☐ Variant known to be disease causing ☐ Variant of unknown significance ☐ Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown *Allele 2:* ☐ Variant known to be disease causing ☐ Variant of unknown significance ☐ Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown
Were variants detected in Other genes? ☐ Yes ☐ No ☐ Don't Know	Check the types of variants found on: *Allele 1:* ☐ Variant known to be disease causing ☐ Variant of unknown significance ☐ Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown *Allele 2:* ☐ Variant known to be disease causing ☐ Variant of unknown significance ☐ Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown

Was enzyme analysis for TFP enzyme activity completed? ☐ Yes ☐ No ☐ Don’t Know	Was enzyme analysis: ☐ Consistent with disease ☐ Normal activity (not consistent with disease) ☐ Unknown
Was functional analysis of fatty acid oxidation in cultured fibroblasts performed? ☐ Yes ☐ No ☐ Don’t Know	Was Functional fibroblast analysis: ☐ Consistent with disease ☐ Normal activity (not consistent with disease) ☐ Unknown

Very Long-chain acyl-CoA Dehydrogenase Deficiency

Case Confirmatory Diagnosis Follow-Up

Instructions: Please answer the questions as fully as possible. All testing refers to confirmatory testing following newborn screening. You may need to consult with relevant clinician(s) and/or medical staff to obtain this information.

Please answer the following as Yes/No/Don't Know	If Yes
Were plasma acylcarnitines tested? ☐ Yes ☐ No ☐ Don't Know	Was C14:1 level ☐ Elevated (on more than one sample) ☐ Normal ☐ Unknown Was C14:2 level ☐ Elevated ☐ Normal ☐ Unknown Was C14 level ☐ Elevated ☐ Normal ☐ Unknown
Was mutation analysis performed for VLCAD? ☐ Yes ☐ No ☐ Don't Know	What genes were included in the mutation analysis? ☐ ACADVL ☐ Other: ___________________

Molecular Genetics Report	
Were variants detected in ACADVL gene? ☐ Yes ☐ No ☐ Don't Know	Check the types of variants found on: *Allele 1:* ☐ Variant known to be disease causing ☐ Variant of unknown significance ☐ Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown *Allele 2:* ☐ Variant known to be disease causing ☐ Variant of unknown significance ☐ Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown
Were variants detected in Other genes? ☐ Yes ☐ No ☐ Don't Know	Check the types of variants found on: *Allele 1:* ☐ Variant known to be disease causing ☐ Variant of unknown significance ☐ Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown *Allele 2:* ☐ Variant known to be disease causing ☐ Variant of unknown significance ☐ Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown
Was enzyme analysis for VLCAD enzyme activity completed? ☐ Yes ☐ No ☐ Don't Know	Was enzyme analysis: ☐ Consistent with disease ☐ Normal activity (not consistent with disease) ☐ Unknown
Was functional analysis of fatty acid oxidation in cultured fibroblasts performed? ☐ Yes ☐ No ☐ Don't Know	Was functional fibroblast analysis: ☐ Consistent with disease ☐ Normal activity (not consistent with disease) ☐ Unknown

Argininosuccinic Acidemia/ Aciduria (ASA)
Case Confirmatory Diagnosis Follow-Up

Instructions: Please answer the questions as fully as possible. All testing refers to confirmatory testing following newborn screening. You may need to consult with relevant clinician(s) and/or medical staff to obtain this information.

Please answer the following as Yes/No/Don't Know	If Yes
Were plasma amino acids tested? ☐ Yes ☐ No ☐ Don't Know	Was plasma ASA level ☐ Elevated ☐ Normal ☐ Unknown Was Citrulline level ☐ Elevated ☐ Normal ☐ Unknown
Were plasma urine acids tested? ☐ Yes ☐ No ☐ Don't Know	Was urine ASA level? ☐ Elevated ☐ Normal ☐ Unknown Was urine Citrulline level? ☐ Elevated ☐ Normal ☐ Unknown
Was a mutation analysis performed for ASA? ☐ Yes ☐ No ☐ Don't Know	What genes were included in the mutation analysis? ☐ ASL ☐ Other gene:_______________

Molecular Genetics Report

Were variants detected in the ASL gene? ☐ Yes ☐ No ☐ Don’t Know	Check the types of variants found on: *Allele 1:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown *Allele 2:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown
Were variants detected in other genes? ☐ Yes ☐ No ☐ Don’t Know	Check the types of variants found on: *Allele 1:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown *Allele 2:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown
Was enzyme analysis for ASA enzyme activity completed? ☐ Yes ☐ No ☐ Don’t Know	Was enzyme activity: ☐ Consistent with disease ☐ Normal activity (not consistent with disease) ☐ Unknown

Citrullinemia Type I (CIT)

Case Confirmatory Diagnosis Follow-Up

Instructions: Please answer the questions as fully as possible. All testing refers to confirmatory testing following newborn screening. You may need to consult with relevant clinician(s) and/or medical staff to obtain this information.

Please answer the following as Yes/No/Don't Know	If Yes
Were plasma amino acids tested? ☐ Yes ☐ No ☐ Don't Know	Was plasma ASA: ☐ Present ☐ Absent ☐ Unknown Was Citrulline level ☐ Elevated ☐ Normal ☐ Unknown
Was blood ammonia tested? ☐ Yes ☐ No ☐ Don't Know	Was blood ammonia level ☐ Elevated ☐ Normal ☐ Unknown
Was a mutation analysis performed for Citrullinemia type I? ☐ Yes ☐ No ☐ Don't Know	What genes were included in the mutation analysis? ☐ ASS1 gene ☐ Other gene:_______________

MOLECULAR GENETICS REPORT	
Were variants detected in the ASS1 gene? ☐ Yes ☐ No ☐ Don’t Know	Check the types of variants found on: *Allele 1:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown *Allele 2:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown
Were variants detected in other genes? ☐ Yes ☐ No ☐ Don’t Know	Check the types of variants found on: *Allele 1:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown *Allele 2:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown
Was enzyme analysis for Cirtullinemia type-I enzyme activity completed? ☐ Yes ☐ No ☐ Don’t Know	Was enzyme activity: ☐ Consistent with disease ☐ Normal activity (not consistent with disease) ☐ Unknown

Cystathionine Beta-Synthase (CBS) Deficiency (Classic Homocystinuria)

Case Confirmatory Diagnosis Follow-Up

Instructions: Please answer the questions as fully as possible. All testing refers to confirmatory testing following newborn screening. You may need to consult with relevant clinician(s) and/or medical staff to obtain this information.

Please answer the following as Yes/No/Don't Know	If Yes
Were plasma amino acids tested? ☐ Yes ☐ No ☐ Don't Know	Was Methionine level ☐ Elevated ☐ Normal ☐ Unknown
Was plasma Homocysteine tested? ☐ Yes ☐ No ☐ Don't Know	Was plasma Homocysteine level ☐ Elevated ☐ Normal ☐ Unknown
Was a mutation analysis performed for CBS? ☐ Yes ☐ No ☐ Don't Know	What genes were included in the mutation analysis? ☐ CBS gene ☐ Other gene:_______________

MOLECULAR GENETICS REPORT	
Were variants detected in the CBS gene? ☐ Yes ☐ No ☐ Don't Know	Check the types of variants found on: *Allele 1:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown *Allele 2:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown
Were variants detected in other genes? ☐ Yes ☐ No ☐ Don't Know	Check the types of variants found on: *Allele 1:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown *Allele 2:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown
Was enzyme analysis for CBS enzyme activity completed? ☐ Yes ☐ No ☐ Don't Know	Was enzyme activity: ☐ Consistent with disease ☐ Normal activity (not consistent with disease) ☐ Unknown

Maple Syrup Urine Disease (MSUD)
Case Confirmatory Diagnosis Follow-Up

Instructions: Please answer the questions as fully as possible. All testing refers to confirmatory testing following newborn screening. You may need to consult with relevant clinician(s) and/or medical staff to obtain this information.

Part I: Final Diagnosis as determined by metabolic geneticist or clinician performing the follow-up

A. MAPLE SYRUP URINE DISEASE, TYPE IA
B. MAPLE SYRUP URINE DISEASE, TYPE IB
C. MAPLE SYRUP URINE DISEASE, TYPE II
D. MAPLE SYRUP URINE DISEASE, TYPE III

Please answer the following as Yes/No/Don't Know	If Yes
Were plasma amino acids tested? ☐ Yes ☐ No ☐ Don't Know	Was Alloisoleucine level ☐ Elevated ☐ Normal ☐ Unknown Was Leucine level ☐ Elevated ☐ Normal ☐ Unknown Was Isoeucine level ☐ Elevated ☐ Normal ☐ Unknown Was Valine level ☐ Elevated ☐ Normal ☐ Unknown Was Leu>Val? ☐ Yes ☐ No ☐ Unknown

Were Urine organic acids tested? ☐ Yes ☐ No ☐ Don't Know	Was 2-ketoisocaproic acid level ☐ Elevated ☐ Normal ☐ Unknown Was 2-OH Isovaleric acid level ☐ Elevated ☐ Normal ☐ Unknown Was 2-ketomethyl valeric acid level ☐ Elevated ☐ Normal ☐ Unknown
Was maternal 3-MCC level tested and ruled out? ☐ Yes ☐ No ☐ Don't Know	[redacted]
Was a mutation analysis performed for MSUD? ☐ Yes ☐ No ☐ Don't Know	What genes were included in the mutation analysis? ☐ *DBT* ☐ *BCKDHB* ☐ *DLD* ☐ *BCKDHA* Other: ________

Molecular Genetics Report

Were variants detected in *DBT*? ☐ Yes ☐ No ☐ Don't Know	Check the types of variants found on: *Allele 1:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown *Allele 2:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown

Were variants detected in *BCKDHD*? ☐ Yes ☐ No ☐ Don't Know	Check the types of variants found on: *Allele 1:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown *Allele 2:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown
Were variants detected in *DLD*? ☐ Yes ☐ No ☐ Don't Know	Check the types of variants found on: *Allele 1:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown *Allele 2:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown
Were variants detected in *BCKDHA*? ☐ Yes ☐ No ☐ Don't Know	Check the types of variants found on: *Allele 1:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown *Allele 2:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown

Were variants detected in Other genes? ☐ Yes ☐ No ☐ Don’t Know	Check the types of variants found on: *Allele 1:* ☐ Variant known to be disease causing ☐ Variant of unknown significance ☐ Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown *Allele 2:* ☐ Variant known to be disease causing ☐ Variant of unknown significance ☐ Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown
Was enzyme analysis for MSUD enzyme activity completed? ☐ Yes ☐ No ☐ Don’t Know	Was enzyme activity: ☐ Consistent with disease ☐ Normal activity (not consistent with disease) ☐ Unknown

Hyperphenylalaninemia (HyperPHE) (Inclusive of Classic PKU)

Case Confirmatory Diagnosis Follow-Up

Instructions: Please answer the questions as fully as possible. All testing refers to confirmatory testing following newborn screening. You may need to consult with relevant clinician(s) and/or medical staff to obtain this information.

Final diagnosis as determined by a metabolic geneticist or clinician performing the follow-up:

Please choose one:

A. Classic PKU
B. Benign HyperPhe
C. HyperPhe diet controlled

Please answer the following as Yes/No/Don't Know	If Yes
Were plasma amino acids tested? ☐ Yes ☐ No ☐ Don't Know	Was Phe level ☐ Elevated (>120umol/L on unrestricted diet) ☐ Normal ☐ Unknown Was Phe/Tyr ratio ☐ Elevated ☐ Normal ☐ Unknown
Were biopterin studies done? ☐ Yes ☐ No ☐ Don't Know	Were biopterin studies: ☐ Normal ☐ Abnormal ☐ Unknown
Was a mutation analysis performed for Hyperphenylalaninemia? ☐ Yes ☐ No ☐ Don't Know	What genes were included in the mutation analysis? ☐ PAH gene ☐ Other gene:_______________

Molecular Genetics Report

Were variants detected in the PAH gene? ☐ Yes ☐ No ☐ Don't Know	Check the types of variants found on: *Allele 1:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown *Allele 2:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown
Were variants detected in other genes? ☐ Yes ☐ No ☐ Don't Know	Check the types of variants found on: *Allele 1:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown *Allele 2:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown
Was enzyme analysis for Hyperphe (inclusive of classic PKU) enzyme activity completed? ☐ Yes ☐ No ☐ Don't Know	Was enzyme activity: ☐ Consistent with disease ☐ Normal activity (not consistent with disease) ☐ Unknown

Tyrosinemia Type I (TYR-1)

Case Confirmatory Diagnosis Follow-Up

Instructions: Please answer the questions as fully as possible. All testing refers to confirmatory testing following newborn screening. You may need to consult with relevant clinician(s) and/or medical staff to obtain this information.

Please answer the following as Yes/No/Don't Know	If Yes
Were plasma organic acids tested? ☐ Yes ☐ No ☐ Don't Know	Was plasma Succinylacetone level ☐ Elevated ☐ Normal ☐ Unknown Was plasma tyrosine level ☐ Elevated ☐ Normal ☐ Unknown
Were urine organic acids tested? ☐ Yes ☐ No ☐ Don't Know	Was urine Succinylacetone level ☐ Elevated ☐ Normal ☐ Unknown Was urine tyrosine level ☐ Elevated ☐ Normal ☐ Unknown
Was mutation analysis performed for Tyrosinemia Type I? ☐ Yes ☐ No ☐ Don't Know	What genes were included in the mutation analysis? ☐ FAH ☐ Other: ___________________

Molecular Genetics Report	

Were variants detected in FAH?
☐ Yes
☐ No
☐ Don’t Know
	Check the types of variants found on:
	Allele 1:
	☐ Variant known to be disease causing
	☐ Variant of unknown significance
	    ☐ Predicted to be pathogenic
	☐ Wild Type (Normal)
	☐ Unknown
	Allele 2:
	☐ Variant known to be disease causing
	☐ Variant of unknown significance
	    ☐ Predicted to be pathogenic
	☐ Wild Type (Normal)
	☐ Unknown

Were variants detected in Other genes?
☐ Yes
☐ No
☐ Don’t Know
	Check the types of variants found on:
	Allele 1:
	☐ Variant known to be disease causing
	☐ Variant of unknown significance
	    ☐ Predicted to be pathogenic
	☐ Wild Type (Normal)
	☐ Unknown
	Allele 2:
	☐ Variant known to be disease causing
	☐ Variant of unknown significance
	    ☐ Predicted to be pathogenic
	☐ Wild Type (Normal)
	☐ Unknown

Was enzyme analysis for Tyrosinemia Type I enzyme activity completed? ☐ Yes ☐ No ☐ Don’t Know	Was enzyme analysis: ☐ Consistent with disease ☐ Normal activity (not consistent with disease) ☐ Unknown

Endocrine Disorders

Congenital Hypothyroidism (CH)

Case Confirmatory Diagnosis Follow-Up

Instructions: Please answer the questions as fully as possible. All testing refers to confirmatory testing following newborn screening. You may need to consult with relevant clinician(s) and/or medical staff to obtain this information.

Final diagnosis as determined by the endocrinologist or clinician performing the follow-up:

Please choose one:

A. Primary Congenital Hypothyroidism
B. Secondary Congenital Hypothyroidism
C. TBG Deficiency (Thyroxine Binding Globulin) or other protein binding defect

Please answer the following as Yes/No/Don't Know	If Yes
Was Serum TSH tested? ☐ Yes ☐ No ☐ Don't Know	What was the level: ☐ TSH > 10 mU/L ☐ TSH 6-10 mU/L ☐ TSH <6 mU/L ☐ Unknown Was it tested before initiation of treatment? ☐ Yes ☐ No ☐ Unknown
Was Serum Total T4 tested? ☐ Yes ☐ No ☐ Don't Know	Was Serum Total T4 below the age-established reference range? ☐ Yes ☐ No ☐ Unknown Was it tested before initiation of treatment? ☐ Yes ☐ No ☐ Unknown
Was Serum Free T4 tested? ☐ Yes ☐ No ☐ Don't Know	Was Serum Free T4 below the age-established reference range? ☐ Yes ☐ No ☐ Unknown Was it tested before initiation of treatment? ☐ Yes ☐ No ☐ Unknown

Does this baby have other pituitary hormone deficiencies? ☐ Yes ☐ No ☐ Don't Know	[redacted]
Does this baby have midline defects? ☐ Yes ☐ No ☐ Don't Know	
Was TBG tested? ☐ Yes ☐ No ☐ Don't Know **Was T3 or T4 resin uptake tested?** ☐ Yes ☐ No ☐ Don't Know	Was TBG below the age established reference range? ☐ Yes ☐ No ☐ Unknown Was T3 or T4 resin uptake above the age established reference range? ☐ Yes ☐ No ☐ Unknown

Congenital Adrenal Hyperplasia (CAH)

Case Confirmatory Diagnosis Follow-Up

Instructions: Please answer the questions as fully as possible. All testing refers to confirmatory testing following newborn screening. You may need to consult with relevant clinician(s) and/or medical staff to obtain this information.

Final diagnosis as determined by the endocrinologist or clinician performing the follow-up:

Please choose one:

A. Classic 21-Hydroxylase Deficiency – Salt Wasting
B. Classic 21-Hydroxylase Deficiency – Simple Virilizing
C. Other Adrenal disorder: (Please list) ___________________

Please answer the following as Yes/No/Don't Know	If Yes
Was a confirmatory serum 17-OHP level obtained? ☐ Yes ☐ No ☐ Don't Know	Was there a value at baseline: ☐ 10,000 ng/dl; ☐ 1000-10,000 ng/dl; ☐ < 1000 ng/dl; ☐ Unknown Was it tested before initiation of treatment? ☐ Yes ☐ No Was there a result after ACTH stimulation: ☐ 10,000 ng/dl; ☐ 1000-10,000 ng/dl; ☐ < 1000 ng/dl; ☐ Unknown Was it tested before initiation of treatment? ☐ Yes ☐ No
Was tandem mass spectrometry urinary steroid profile obtained? ☐ Yes ☐ No ☐ Don't Know	Were the urinary spectrometry steroid profile results: ☐ Indicative of 21-Hydroxylase Deficiency CAH ☐ Unknown

Was serum sodium level measured before initiation of treatment? ☐ Yes ☐ No ☐ Don't Know	Was the sodium level: ☐ < 135 mEq/L ☐ > 135 mEq/L ☐ Unknown Was it tested before initiation of treatment? ☐ Yes ☐ No
Was Plasma renin activity level measured at time of initiation of treatment? ☐ Yes ☐ No ☐ Don't Know	Was the Plasma renin activity normal for age? ☐ Yes ☐ No Was it tested before initiation of treatment? ☐ Yes ☐ No

MOLECULAR GENETICS REPORT

Was mutation analysis for 21-Hydroxylase deficiency (*CYP21A2*) performed? ☐ Yes ☐ No ☐ Don't Know	Check the types of variants found on: *Allele 1:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown *Allele 2:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown

CLINICAL RESULTS

Is there evidence of salt wasting? (e.g. shock or severe failure to thrive)? ☐ Yes ☐ No ☐ Don't Know	[redacted]
Is there supportive clinical or laboratory evidence of CAH? ☐ Yes ☐ No ☐ Don't Know	Is the evidence: (check all that apply) ☐ Ambiguous genitalia, with 46,XX karyotype ☐ Normal genitalia, with 46,XY karyotype ☐ Other hormonal evidence of CAH

Hemoglobinopathies

Presence of Hb S

Case Confirmatory Diagnosis Follow-Up

Instructions: Please answer the questions as fully as possible. All testing refers to confirmatory testing following newborn screening. You may need to consult with relevant clinician(s) and/or medical staff to obtain this information

Please answer the following:	If Yes
Final Diagnosis as determined by a clinician performing the follow-up ☐ S, Beta + Thalassemia – Hb S/B + Th ☐ S, C disease – Hb S/C ☐ *Sickle Cell Disease, Hb S only* ☐ S,S Disease (Sickle Cell Anemia) – Hb SS ☐ S, Beta 0-thalassemia – Hb S/B0Th ☐ Not Known ☐ S, other	
Was qualitative (IEF or HPLC) testing completed? ☐ Yes ☐ No ☐ Unknown	What were the results? ☐ FS ☐ FSC ☐ FSA ☐ FSA$_2$ ☐ FSAA$_2$ ☐ Other ☐ Unknown
Was quantitative (HPLC or electrophoresis) testing completed? ☐ Yes ☐ No ☐ Unknown	What were the results? ☐ FS ☐ FSC ☐ FS with high A$_2$ ☐ FSA with high A$_2$ ☐ FSA ☐ Other ☐ Unknown

Was mutation analysis performed? ☐ Yes ☐ No ☐ Unknown	Check the type of variant found on allele 1: ☐ S ☐ C ☐ Beta + Thal ☐ Beta^0 Thal ☐ Other ☐ Unknown Check the type of variant found on allele 2: ☐ S ☐ C ☐ Beta + Thal ☐ Beta^0 Thal ☐ Other ☐ Unknown
NBS result ☐ Yes ☐ No ☐ Unknown	What were the results? ☐ FS ☐ FSC ☐ FSA ☐ FSA$_2$ ☐ Other ☐ Unknown
Was a CBC performed? ☐ Yes ☐ No ☐ Unknown	What were the results? ☐ Normal – high MCV ☐ Low MCV ☐ Unknown
Were family studies (in parents) done? ☐ Yes ☐ No ☐ Unknown	What were the results? Maternal Status: ☐ Carrier S ☐ Carrier C ☐ Carrier Beta + Thal ☐ Carrier Beta^0 Thal ☐ Other ☐ Unknown Paternal Status: ☐ Carrier S ☐ Carrier C ☐ Carrier Beta + Thal ☐ Carrier Beta^0 Thal ☐ Other ☐ Unknown

Was there a positive family history? ☐ Yes ☐ No ☐ Unknown	
Were HPLC & IEF tested on the same sample from the infant? ☐ Yes ☐ No ☐ Unknown	What were the results? ☐ FS ☐ FSC ☐ FSA_2 ☐ $FSAA_2$ ☐ Other ☐ Unknown
Were Hgb tests (electrophoresis or HPLC) performed on family members? ☐ Yes ☐ No ☐ Unknown	What were the results? ☐ Positive ☐ Negative ☐ Unknown

Presence of Other Hb Variant

Case Confirmatory Diagnosis Follow-Up

Instructions: Please answer the questions as fully as possible. All testing refers to confirmatory testing following newborn screening. You may need to consult with relevant clinician(s) and/or medical staff to obtain this information.

Please answer the following:	If Yes
Final Diagnosis as determined by a clinician performing the follow-up ☐ Hemoglobin C disease ☐ Hemoglobin D disease ☐ Hemoglobin E disease ☐ Hemoglobin O-Arab disease ☐ Other hemoglobin disease, please describe	
Alpha thalassemia present? ☐ Yes ☐ No ☐ Unknown	
Was qualitative (IEF or HPLC) testing completed? ☐ Yes ☐ No ☐ Unknown	What were the results? ☐ FC ☐ FD ☐ FE ☐ FO_{ARAB} ☐ Other ☐ Unknown
Was quantitative (HPLC or electrophoresis) testing completed? ☐ Yes ☐ No ☐ Unknown	What were the results? ☐ FC ☐ FD ☐ FE ☐ FO_{ARAB} ☐ Other ☐ Unknown

Was mutation analysis performed? ☐ Yes ☐ No ☐ Unknown	Check the type of variant found on allele 1: ☐ C ☐ D ☐ E ☐ O-Arab ☐ Other ☐ Unknown Check the type of variant found on allele 2: ☐ C ☐ D ☐ E ☐ O-Arab ☐ Beta + Thal ☐ Beta^0 Thal ☐ Other ☐ Unknown
NBS result ☐ Yes ☐ No ☐ Unknown	What were the results? ☐ FC ☐ FD ☐ FE ☐ FO$_{ARAB}$ ☐ Other ☐ Unknown
Was a CBC performed? ☐ Yes ☐ No ☐ Unknown	What were the results? ☐ Normal – high MCV ☐ Low MCV ☐ Unknown

Were family studies (in parents) done? ☐ Yes ☐ No ☐ Unknown	What were the results? Maternal Status: ☐ Carrier C ☐ Carrier D ☐ Carrier E ☐ Carrier O-Arab ☐ Carrier Beta + Thal ☐ Carrier Beta^0 Thal ☐ Other ☐ Unknown Paternal Status: ☐ Carrier C ☐ Carrier D ☐ Carrier E ☐ Carrier O-Arab ☐ Carrier Beta + Thal ☐ Carrier Beta^0 Thal ☐ Other ☐ Unknown
Was there a positive family history? ☐ Yes ☐ No ☐ Unknown	
Were Hgb tests (electrophoresis or HPLC) performed on family members? ☐ Yes ☐ No ☐ Unknown	What were the results? ☐ Positive ☐ Negative ☐ Unknown

Mucopolysaccharidosis Type I (MPS I)

Case Confirmatory Diagnosis Follow-Up

Birth weight (grams):

Gestational age (weeks gestation at time of birth):

State of birth (state reporting the case):

Sex (male/female/unknown):

Instructions: Please answer the questions as fully as possible. All testing refers to confirmatory testing following newborn screening. You may need to consult with relevant clinician(s) and/or medical staff to obtain this information.

Final diagnosis as determined by a metabolic geneticist or clinician performing follow-up:

Please choose one:

1. Primary targets of NBS
    a. MPS I –severe
    b. MPS I – severity not determined
    c. MPS I – attenuated

Please answer the following as Yes/No/Unknown	If Yes
Was enzyme activity tested? ☐ Yes ☐ No ☐ Unknown	What was the enzyme level? ☐ Within lab known affected range ☐ Unknown
Were urine GAGS tested? ☐ Yes ☐ No ☐ Unknown	What was the urine GAG level? ☐ Elevated ☐ Normal ☐ Unknown

Clinical symptoms/ lab findings? ☐ Symptoms present and documented by specialists. Public health (PH) program continued to collect data through the development of symptoms ☐ No symptoms by the time the PH Program closes follow-up (either due to child being lost to follow-up OR program policy on follow-up time ☐ Unknown	*Clinical symptoms consistent with MPS-I include: Hepatosplenomegaly, Coarse facial features, Hydrocephalus, Skeletal deformities (dysostosis multiplex), Corneal clouding, Large tongue, Prominent forehead, Joint stiffness, Short stature, frequent ear infections and hearing loss, hernia*
MOLECULAR GENETICS REPORT	
Were variants detected in the genes known to be associated with MPS I? ☐ Yes ☐ No ☐ Unknown	Check the types of variant(s) found on: Allele 1: ☐ Pathogenic variant and associated with SEVERE disease ☐ Pathogenic or likely pathogenic variant ☐ Variant known to be associated with ATTENUATED Disease ☐ Wild Type (Normal) ☐ Untested/Unknown Allele 2: ☐ Pathogenic variant and associated with SEVERE disease ☐ Pathogenic or likely pathogenic variant ☐ Variant of uncertain significance ☐ Variant known to be associated with ATTENUATED Disease ☐ Wild Type (Normal) ☐ Untested/Unknown

Pompe Disease
Case Confirmatory Diagnosis Follow-Up

Birth weight (grams):

Gestational age (weeks gestation at time of birth):

State of birth (state reporting the case):

Sex (male/female/unknown):

Instructions: Please answer the questions as fully as possible. All testing refers to confirmatory testing following newborn screening. You may need to consult with relevant clinician(s) and/or medical staff to obtain this information.

Final diagnosis as determined by metabolic geneticist or clinician performing the follow-up:

Please choose one:

1. Primary targets of NBS
    a. Infantile Onset (IO) Pompe Disease
    b. Late Onset (LO) Pompe Disease

Please answer the following as Yes/No/Don't Know	If Yes
Was enzyme activity tested in blood (not DBS sample)? ☐ Yes ☐ No ☐ Unknown	What was the enzyme level? ☐ Within lab known affected range for infantile onset (IO) ☐ Low (above affected range for IO, may or may not be in late-onset (LO) range but should not be above LO range)) ☐ Within lab known affected range for late onset (LO) ☐ Low (above affected range, for LO not normal) ☐ Unknown
Was enzyme activity tested in skin/muscle? ☐ Yes ☐ No ☐ Unknown	☐ Positive skin or muscle biopsy ☐ Unknown
Was there Cardiac involvement consistent with Pompe? ☐ Yes ☐ No ☐ Unknown	☐ Positive findings on Chest X-ray/EKG/ECHO in newborn period ☐ Positive findings on Chest X-ray/EKG/ECHO

Lab findings? ☐ Elevated CK/AST/ALT/LDH/Urine Hex4 ☐ Not present ☐ Unknown ☐ Not done	
Clinical findings? ☐ Symptoms present after 1 year of age and documented by specialists. PH program continued to collect data through the development of symptoms ☐ Symptoms present before 1 year of age but no cardiac involvement ☐ Unknown or not reported to PH by the end of follow-up	*Clinical symptoms consistent with Pompe Disease: progressive muscle weakness, need for respiratory assistance, swaying gait or waddle, Lordosis, kyphosis, or scoliosis*
Molecular Genetics Report	
Were variants detected in the genes known to be associated with Pompe Disease? ☐ Yes ☐ No ☐ Unknown	Check the types of variant(s) found on: Allele 1: ☐ Pathogenic ☐ Pathogenic variant and associated with infantile onset ☐ Novel variant that is likely pathogenic ☐ Pathogenic variant or likely pathogenic variant, with deletion or duplication consistent with infantile onset ☐ Pathogenic and associated with non-classical disease, or variant of uncertain significance ☐ Pathogenic or likely pathogenic variant, no other variants found, dup/del testing not done or not known ☐ Pathogenic or likely pathogenic variant, no other variants found ☐ Wild Type (Normal) ☐ Unknown Allele 2: ☐ Pathogenic ☐ Pathogenic variant and associated with infantile onset ☐ Novel variant that is likely pathogenic ☐ Pathogenic variant or likely pathogenic variant, with deletion or duplication consistent with infantile onset ☐ Pathogenic and associated with non-classical disease, or variant of uncertain significance ☐ Pathogenic or likely pathogenic variant, no other variants found, dup/del testing not done or not known ☐ Pathogenic or likely pathogenic variant, no other variants found ☐ Wild Type (Normal) ☐ Unknown

Other Disorders

Biotinidase Deficiency

Case Confirmatory Diagnosis Follow-Up

Instructions: Please answer the questions as fully as possible. All testing refers to confirmatory testing following newborn screening. Attach a copy of the laboratory reports supporting these findings. The reports will be stored within the newborn screening program for future reference.

Final Diagnosis as determined by metabolic geneticist or clinician performing the follow-up

D. Profound Biotinidase deficiency
E. Partial Biotinidase deficiency

Was enzyme analysis for biotinidase enzyme activity completed? ☐ Yes ☐ No ☐ Don't Know	What as the enzyme activity? ☐ <10% normal activity ☐ 10-30% normal activity ☐ Normal ☐ Unknown
Was mutation analysis performed for Biotinidase deficiency? ☐ Yes ☐ No ☐ Don't Know	Check the types of variants found on: *Allele 1:* ☐ Variant known to be disease causing ☐ Known to be associated with profound enzyme deficiency ☐ Known to be associated with partial enzyme deficiency [‘mild’ mutation (D444H)] ☐ Variant of unknown significance ☐ Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown *Allele 2:* ☐ Variant known to be disease causing ☐ Known to be associated with profound enzyme deficiency ☐ Known to be associated with partial enzyme deficiency [‘mild’ mutation (D444H)] ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) Unknown

Galactosemia

Case Confirmatory Diagnosis Follow-Up

Instructions: Please answer the questions as fully as possible. All testing refers to confirmatory testing after newborn screening. Attach a copy of the laboratory reports supporting these findings. The reports will be stored within the newborn screening program for future reference.

Please answer the following as Yes/No/Don't Know	If Yes
Were GALT levels tested? ☐ Yes ☐ No ☐ Don't Know	Was GALT level ☐ <10% ☐ 10-30% ☐ Normal ☐ Unknown
Were Gal-1-P tested? ☐ Yes ☐ No ☐ Don't Know	Was Gal-1-P level ☐ Elevated ☐ Normal ☐ Unknown
Was Urine Galactitol tested? ☐ Yes ☐ No ☐ Don't Know	Was Gal-1-P level ☐ Elevated ☐ Normal ☐ Unknown
Was a mutation analysis performed for Galactosemia? ☐ Yes ☐ No ☐ Don't Know	Check the types of variants found on: *Allele 1:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown *Allele 2:* ☐ Variant known to be disease causing ☐ Variant of unknown significance o Predicted to be pathogenic ☐ Wild Type (Normal) ☐ Unknown
If Variant Galactosemia, was protein phenotyping completed? ☐ Yes ☐ No ☐ Don't Know ☐ N/A	Did result indicate ☐ phenotype consistent with variant ☐ phenotype NOT consistent with variant ☐ Unknown

If Arginase Deficiency, were enzyme studies completed? ☐ Yes ☐ No ☐ Don’t Know ☐ N/A	Was enzyme activity: ☐ Consistent with disease ☐ Normal activity (not consistent with disease) ☐ Unknown

Cystic Fibrosis

Case Confirmatory Diagnosis Follow-Up

Instructions: Please answer the questions as fully as possible. All testing refers to confirmatory testing following newborn screening. Attach a copy of the laboratory reports supporting these findings. The reports will be stored within the newborn screening program for future reference.

Please choose one:

D. Typical Cystic Fibrosis (CF)
E. CFTR-Related Metabolic Syndrome (CRMS)
F. CFTR-Related Disease

Please answer the following as Yes/No/Don't Know	**If Yes**
Did the NBS result indicate an elevated IRT? ☐ Yes ☐ No ☐ Don't Know	
Were CFTR mutations detected on the **newborn screening** mutation panel? ☐ Yes ☐ No ☐ Don't Know (* Mutations seen in patients with CF have been classified as disease-causing, neutral, or varying clinical consequences through the CFTR2 project: http://cftr2.org/browse.php. Additional information about the mutation and the association with lower sweat chlorides can also be found at CFTR2.)	Check the types of variants found on: *Allele 1:* ☐ Variant known to be disease causing in CFTR2 ☐ Shown to be associated with lower sweat chlorides ☐ Neutral variant ☐ Variant of varying clinical consequence in CFTR2 ☐ Wild Type (Normal) ☐ Unknown (not reported in CFTR2) *Allele 2:* ☐ Variant known to be disease causing in CFTR2 ☐ Shown to be associated with lower sweat chlorides ☐ Neutral variant ☐ Variant of varying clinical consequence in CFTR2 ☐ Wild Type (Normal) ☐ Unknown (not reported in CFTR2)
Did the child have meconium ileus? ☐ Yes ☐ No ☐ Don't Know	

Was a valid sweat chloride result available? ☐ Yes ☐ No ☐ Don't Know	What were the sweat test results (please report the highest sweat chloride value from one sweat test)? ☐ >=60 mmol/L (regardless of age) If <60 mmol/L If age< 6 months ☐ <30 mmol/L ☐ 30-59 mmol/L If age≥6 months ☐ <40 mmol/L ☐ 40 -59 mmol/L ☐ Quantity Not Sufficient
If a valid sweat test was not available, were there attempts to obtain a sweat chloride that were quantity not sufficient (QNS)? ☐ Yes ☐ No ☐ Don't Know	
Was a sweat chloride repeated on a separate day (results from different arm on the same day should not be reported here)? ☐ Yes ☐ No ☐ Don't Know	What were the repeat sweat test results (please report the highest sweat chloride value from one sweat test)? ☐ >=60 mmol/L (regardless of age) If <60 mmol/L If age< 6 months ☐ <30 mmol/L ☐ 30-59 mmol/L If age≥6 months ☐ <40 mmol/L ☐ 40 -59 mmol/L

Was a CFTR mutation panel completed after the newborn screening mutation panel? ☐ Yes ☐ No ☐ Don't Know (* Mutations seen in patients with CF have been classified as disease-causing, neutral, or varying clinical consequences through the CFTR2 project: http://cftr2.org/browse.php. Additional information about the mutation and the association with lower sweat chlorides can also be found at CFTR2.)	Check the types of variants found on: *Allele 1:* ☐ Variant known to be disease causing in CFTR2 ☐ Shown to be associated with lower sweat chlorides ☐ Neutral variant ☐ Variant of varying clinical consequence in CFTR2 ☐ Wild Type (Normal) ☐ Unknown (not reported in CFTR2) *Allele 2:* ☐ Variant known to be disease causing in CFTR2 ☐ Shown to be associated with lower sweat chlorides ☐ Neutral variant ☐ Variant of varying clinical consequence in CFTR2 ☐ Wild Type (Normal) ☐ Unknown (not reported in CFTR2)

Question Below to be answered only if child was diagnosed after the newborn period

If child was diagnosed after the newborn period, were clinical symptoms associated with CFTR Related Disease present? ☐ Yes ☐ No ☐ Don't Know	Symptoms include: ☐ CBAVD ☐ Recurrent pancreatitis ☐ Nasal polyposis ☐ Infertility ☐ Focal biliary cirrhosis with portal hypertension

Summary of common variants as reported on CFTR2 (this is not an exhaustive list; please visit www.CFTR2.org for the latest updated list).

Variant name - HGVS nomenclature	Protein name	Variant legacy name	On ACMG Screening Panel	CFTR2 final call	Associated with lower sweat chloride
c.3717+12191C>T	p.Phe316LeufsX12	**1078delT**	No	CF-causing	NO
c.579+3A>G	p.Phe342HisfsX28	**1154insTC**	No	CF-causing	NO
c.3454G>C	No protein name	**1717-1G->A**	Yes	CF-causing	NO
c.3208C>T	No protein name	**1811+1.6kbA->G**	No	CF-causing	NO
c.3154T>G	No protein name	**1898+1G->A**	Yes	CF-causing	NO
c.1585-1G>A	p.Leu671X	**2143delT**	No	CF-causing	NO
c.1680-1G>A	p.Lys684SerfsX38	**2183AA->G**	No	CF-causing	NO
c.1766+1G>A	p.Lys684AsnfsX38	**2184delA**	Yes	CF-causing	NO
c.2490+1G>A	p.Gln685ThrfsX4	**2184insA**	No	CF-causing	NO
c.2988+1G>A	p.Glu726ArgfsX4	**2307insA**	No	CF-causing	NO
c.1736A>G	No protein name	**2789+5G->A**	Yes	CF-causing	NO
c.1408A>G	No protein name	**3120+1G->A**	Yes	CF-causing	NO
c.1841A>G	No protein name	**3120G->A**	No	CF-causing	NO
c.2991G>C	No protein name	**3272-26A->G**	No	CF-causing	NO
c.489+1G>T	p.Lys1177SerfsX15	**3659delC**	Yes	CF-causing	NO
c.350G>A	No protein name	**3849+10kbC->T**	Yes	CF-causing	NO
c.4242+1G>T	p.Leu1258PhefsX7	**3905insT**	No	CF-causing	NO
c.3718-1G>A	p.Leu88IlefsX22	**394delTT**	No	CF-causing	NO
c.1240C>T	No protein name	**5T**	No	Indeterminate	YES
c.2260G>A	No protein name	**621+1G->T**	Yes	CF-causing	NO
c.1727G>C	No protein name	**711+1G->T**	Yes	CF-causing	NO
c.220C>T	No protein name	**711+5G->A**	No	CF-causing	NO
c.2834C>T	p.Ala455Glu	**A455E**	Yes	CF-causing	NO
c.1675G>A	p.Ala559Thr	**A559T**	No	CF-causing	NO
c.1127_1128insA	p.Ser18ArgfsX16	**CFTRdele2,3**	No	CF-causing	NO
c.1202G>A or c.1203G>A	p.Asp1152His	**D1152H**	No	Indeterminate	YES
c.1923_1931del9insA	p.Glu60X	**E60X**	No	CF-causing	NO
c.1679G>C	p.Phe508del	**F508del**	Yes	CF-causing	NO
c.3160C>G	p.Gly1244Glu	**G1244E**	No	CF-causing	NO
c.4046G>A	p.Gly178Glu	**G178R**	No	CF-causing	NO
c.4196_4197delTC	p.Gly542X	**G542X**	Yes	CF-causing	NO
c.3731G>A	p.Gly551Asp	**G551D**	Yes	CF-causing	NO
c.3197G>A	p.Gly85Glu	**G85E**	Yes	CF-causing	NO
c.2657+2_2657+3insA	p.Ile1027Thr	**I1027T**	No	Not CF-causing	NO
c.1673T>C	p.Ile148Thr	**I148T**	No	Not CF-causing	NO

c.3763T>C	p.Ile336Lys	**I336K**	No	CF-causing	NO
c.1558G>T	p.Ile507del	**I507del**	Yes	CF-causing	NO
c.3230T>C	p.Leu1077Pro	**L1077P**	No	CF-causing	NO
c.1040G>A	p.Leu206Trp	**L206W**	No	CF-causing	NO
c.3302T>A	p.Met1101Lys	**M1101K**	No	CF-causing	NO
c.274G>A	p.Asn1303Lys	**N1303K**	Yes	CF-causing	NO
c.617T>G	p.Pro67Leu	**P67L**	No	CF-causing	NO
c.2764_2765insAG	p.Gln220X	**Q220X**	No	CF-causing	NO
c.1973_1985del13insAGAAA	p.Gln493X	**Q493X**	No	CF-causing	NO
c.3196C>T	p.Arg1066Cys	**R1066C**	No	CF-causing	NO
c.4296_4297insGA	p.Arg1158X	**R1158X**	No	CF-causing	NO
c.1692delA	p.Arg1162X	**R1162X**	Yes	CF-causing	NO
c.1055G>A	p.Arg117Cys	**R117C**	No	CF-causing	NO
c.1466C>A	p.Arg117His	**R117H**	Yes	Indeterminate	YES
c.1013C>T	p.Arg334Trp	**R334W**	Yes	CF-causing	NO
c.532G>A	p.Arg347His	**R347H**	Yes	CF-causing	NO
c.1040G>C	p.Arg347Pro	**R347P**	No	CF-causing	NO
c.2908G>C	p.Arg352Gln	**R352Q**	No	CF-causing	NO
c.2424_2425insAT	p.Arg553X	**R553X**	Yes	CF-causing	NO
c.2780T>C	p.Arg560Thr	**R560T**	Yes	CF-causing	NO
c.349C>T	p.Ser1251Asn	**S1251N**	No	CF-causing	NO
c.1000C>T	p.Ser549Asn	**S549N**	No	CF-causing	NO
c.3752G>A	p.Ser945Leu	**S945L**	No	CF-causing	NO
c.1645A>C or c.1647T>G	p.Val520Phe	**V520F**	No	CF-causing	NO
c.274G>T	p.Trp1282X	**W1282X**	Yes	CF-causing	NO
c.2128A>T	p.Tyr1092X	**Y1092X**	No	CF-causing	NO
c.2195T>G	p.Tyr122X	**Y122X**	No	CF-causing	NO

Severe Combined Immunodeficiencies
Case Confirmatory Diagnosis Follow-Up

Birth weight (grams): __________

Gestational age (weeks gestation at time of birth): __________

State of birth (state reporting the case): __________

Sex (male/female/unknown): __________

Instructions: Please answer the questions as fully as possible. All testing refers to confirmatory testing following newborn screening. You may need to consult with relevant clinician(s) and/or medical staff to obtain this information.

Final diagnosis as determined by a metabolic geneticist or clinician performing the follow-up:

Please choose one:

1. Primary targets of NBS
   a. Classic SCID
   b. Leaky SCID
   c. Omenn Syndrome

Please answer the following as Yes/No/Don't Know	If Yes
Was the CD3 T cell level tested? ☐ Yes ☐ No ☐ Unknown/untested	What was the CD3 T cell level? ☐ <300 autologous T cells, undetectable or very few naïve T cells ☐ 300-1500, few naïve T cells, oligoclonal T cells or poor T cell diversity ☐ >80% CD45RO+ ☐ Any number (not zero) ☐ Untested/Unknown
Was proliferation to PHA test done? ☐ Yes ☐ No ☐ Unknown/untested	Proliferation to PHA: ☐ <10% of normal ☐ 10-50% of normal PHA ☐ 10-30% normal PHA or Absent to Candida/TT ☐ <30% of normal ☐ Any/Unknown

Was Maternal engraftment documented? ☐ **Yes** ☐ **No** ☐ **Unknown/Untested**	
Was a mutation analysis performed in the genes known to be associated with SCID? ☐ Yes ☐ No ☐ Unknown/untested	
Molecular Genetics Report	
Were variants detected in the genes known to be associated with SCID? ☐ Yes ☐ No ☐ Unknown/untested	Check the types of variant(s) found on: Allele 1: ☐ Pathogenic variant in a known SCID gene ☐ Pathogenic variant in a known SCID gene on X chromosome in a male ☐ Pathogenic variant in a known SCID gene known to be associated with leaky SCID (previously reported or in a gene previously associated with combined immunodeficiency) ☐ Wild Type (Normal) ☐ Untested/Unknown Allele 2: ☐ Pathogenic variant in a known SCID gene ☐ Pathogenic variant in a known SCID gene known to be associated with leaky SCID (previously reported or in a gene previously associated with immunodeficiency) ☐ Wild Type (Normal) ☐ Untested/Unknown
	Was 22q11 deletion ruled out? ☐ Yes ☐ No ☐ Don’t Know

	Were homozygous or compound heterozygous FOXN1 mutations ruled out? ☐ **Yes** ☐ **No** ☐ **Don’t Know**
	Were heterozygous TBX1 variants ruled out? ☐ **Yes** ☐ **No** ☐ **Don’t Know**

Critical Congenital Heart Disease

Case Confirmatory Diagnosis Follow-Up

Instructions: Please answer the questions as fully as possible. All testing refers to confirmatory testing following newborn screening. Attach a copy of the laboratory reports supporting these findings. The reports will be stored within the newborn screening program for future reference.

What was the Final Diagnosis? (Check all that apply)

- ☐ CCHD (Specify)
    - ☐ Truncus Arteriosus
    - ☐ Total Anomalous Pulmonary Venous Connection
    - ☐ Tetralogy of Fallot
    - ☐ Pulmonary Atresia
    - ☐ Ebstein's Anomaly
    - ☐ Hypoplastic Left Heart Syndrome
    - ☐ Single Ventricle
    - ☐ Tricuspid Atresia
    - ☐ Transposition of the Great Arteries
    - ☐ Double Outlet Right Ventricle
    - ☐ Coarctation of Aorta
    - ☐ Interrupted Arch
    - ☐ Aortic Valve Disease
- ☐ Non critical CHD (Please specify)
- ☐ Other (Please specify)

Please answer the following:	If Yes, what were the results of the echocardiogram?
Was a Postnatal Echocardiogram Completed? ☐ Yes ☐ No ☐ Unknowm/untested	**Truncus Arteriosus** ☐ Truncus arteriosus ☐ Truncus arteriosus + Interrupted aortic arch
	Total Anomalous Pulmonary Venous Connection (TAPVC) ☐ Type1 (supracardiac) ☐ Type 2 (cardiac) ☐ Type 3 (infracardiac) ☐ Type 4 (mixed)
	Tetralogy of Fallot (TOF) ☐ TOF ☐ TOF, Pulmonary stenosis ☐ TOF, AVCanal (AVSD) ☐ TOF, Absent pulmonary valve ☐ Interrupted aortic arch + AP window (aortopulmonary window)
	Pulmonary Artesia ☐ Pulmonary atresia ☐ Pulmonary atresia, IVS ☐ Pulmonary atresia, VSD (Including TOF, PA) ☐ Pulmonary atresia, VSD-MAPCA
	Ebstein's Anomaly ☐ Ebstein's anomaly
	Hypoplastic Left Heart Syndrome (HLHS) ☐ Hypoplastic left heart syndrome
	Single Ventricle ☐ Single ventricle, DILV ☐ Single ventricle, DIRV ☐ Single ventricle, Mitral atresia ☐ Single ventricle, Unbalanced AV canal ☐ Single ventricle, Heterotaxia syndrome ☐ Single ventricle, Other ☐ Single ventricle + Total anomalous pulmonary venous connection (TAPVC)
	Tricuspid Artesia ☐ Single ventricle, Tricuspid atresia
	Transposition of the Great Arteries (TGA) ☐ d-TGA, IVS ☐ d-TGA, IVS-LVOTO ☐ d-TGA, VSD ☐ d-TGA, VSD-LVOTO

	Double Outlet Right Ventricle (DORV) ☐ DORV, VSD type ☐ DORV, TOF type ☐ DORV, TGA type	☐ DORV, Remote VSD (uncommitted VSD) ☐ DORV + AVSD (AV Canal) ☐ DORV, IVS
	Coarctation of Aorta ☐ Coarctation of aorta ☐ Aortic arch hypoplasia ☐ VSD + Aortic arch hypoplasia ☐ VSD + Coarctation of aorta	
	Interrupted Arch ☐ Interrupted aortic arch ☐ Interrupted aortic arch + VSD ☐ Interrupted aortic arch + AP window (aortopulmonary window)	
	Aortic Valve Disease ☐ Aortic Stenosis receiving intervention in first 30 days of life ☐ Pulmonary Stenosis receiving intervention in the first 30 days of life	
Please answer the following:	**If Yes**	
Was a Prenatal Echocardiogram Completed? ☐ Yes ☐ No ☐ Don't Know	Did the Prenatal Echo findings suggest CCHD? ☐ Yes ☐ No	

X-Linked Adrenoleukodystrophy (X-ALD)

Case Confirmatory Diagnosis Follow-Up

Birth weight (grams):

Gestational age (weeks gestation at time of birth):

State of birth (state reporting the case):

Sex (male/female/unknown):

Instructions: Please answer the questions as fully as possible. All testing refers to confirmatory testing following newborn screening. You may need to consult with relevant clinician(s) and/or medical staff to obtain this information.

Final diagnosis as determined by a metabolic geneticist or clinician performing the follow-up:

Please choose one:

1. Primary targets of NBS
    a. X-Linked Adrenoleukodystrophy (in Males)
    b. Contiguous ABCD1 DXS1357E deletion syndrome (CADDS)
    c. X-Linked Adrenoleukodystrophy (in Females)
    d. Zellweger Spectrum Disorder
    e. Peroxisomal Disorder
    f. Acyl-CoA Oxidase Deficiency
    g. D-Bifunctional Protein Deficiency
    h. Dyamin-like protein 1 (DLP1)
    i. ABDC5
    j. Non-peroxisomal Disorder

Please answer the following as Yes/No/Don't Know	If Yes
Was plasma VLCFA tested? ☐ Yes ☐ No ☐ Unknown	What was the VLCFA level? ☐ Elevated ☐ Slightly elevated ☐ Normal ☐ Low ☐ Unknown
Clinical symptoms? ☐ Present ☐ Not present ☐ Not present at birth ☐ Unknown/ Not available	*Symptoms may include: neonatal hypotonia, neonatal seizures, liver disease, neonatal cholestasis, sensorineural deafness, failure to thrive, craniofacial abnormalities*
Was plasmalogen testing done? ☐ Yes ☐ No ☐ Unknown	Plasmalogen level? ☐ Normal ☐ Low ☐ Unknown/ Not available
Family History done? ☐ Yes ☐ No ☐ Unknown	Family history results: ☐ Family history present or family VLCFA studies suggestive of X-linked ALD ☐ Unknown
Were fibroblast studies done? ☐ Yes ☐ No ☐ Unknown	Fibroblast study results: ☐ Consistent with Zellweger Spectrum Disorder ☐ Consistent with Acyl-CoA Oxidase Deficiency ☐ Consistent with D-Bifunctional Protein ☐ Consistent with DLP1 ☐ Consistent with ABCD5 ☐ Unknown
MOLECULAR GENETICS REPORT	
Were variants detected in the ABCD1 gene? ☐ Yes ☐ No ☐ Unknown/untested	Check the types of variant(s) found: ☐ Pathogenic variant ☐ Deletion/ duplication identified ☐ No mutation on sequencing, deletion/duplication not done ☐ No mutation on sequencing, deletion/duplication not done; rule out other disorders of peroxisomal beta oxidation ☐ Variant of uncertain significance ☐ Deletion identified in ABCD1 and DXS1357E ☐ Unknown

Were variants detected in the PEX1 gene? ☐ Yes ☐ No ☐ Unknown/untested	Check the types of variant(s) found: ☐ Two pathogenic variants in the PEX1 gene ☐ Unknown
Were variants detected in the ACOX1 gene? ☐ Yes ☐ No ☐ Unknown/untested	Check the types of variant(s) found: ☐ Two pathogenic mutations in the ACOX1 gene ☐ Unknown
Were variants detected in the HSD17B4 gene? ☐ Yes ☐ No ☐ Unknown/untested	Check the types of variant(s) found: ☐ Two pathogenic mutations in the HSD17B4 gene ☐ Unknown
Mutational analysis done on other genes? ☐ Yes ☐ No ☐ Unknown/untested	Check the types of variant(s) found: ☐ No mutation on sequencing, deletion/duplication not found ☐ Heterozygous, dominant-negative ☐ Two disease causing mutations ☐ Mutation in one of the 7 known genes for Aicardi-Goutiéres Syndrome ☐ Unknown

Spinal Muscular Atrophy (SMA)
Case Confirmatory Diagnosis Follow-Up

Birth weight (grams): ____________________

Gestational age (weeks gestation at time of birth): ____________________

State of birth (state reporting the case): ____________________

Sex (male/female/unknown): ____________________

Instructions: Please answer the questions as fully as possible. All testing refers to confirmatory testing following newborn screening. You may need to consult with relevant clinician(s) and/or medical staff to obtain this information.

Final diagnosis as determined by a metabolic geneticist or clinician performing the follow-up:

Please answer the following as Yes/No/Don't Know	If Yes
Newborn Screen Molecular Test for SMN1? ☐ Yes ☐ No ☐ Unknown	What was the result? ☐ Zero copies of SMN1 (presumed homozygous deletion/conversion)* ☐ Zero copies of SMN1 (presumed homozygous deletion/conversion)* - observed on two independently collected NBS specimens ☐ 2 pathogenic variants ☐ 2 pathogenic variants observed on two independently collected NBS specimens ☐ 1 pathogenic variant and 1 variant of unknown significance ☐ 2 variants of unknown significance ☐ Unknown/ Not Done/Screen Negative
Newborn Screen Molecular Test for SMN2? ☐ Yes ☐ No ☐ Unknown	SMN2 Copy Number? ☐ One ☐ Two ☐ Two or more ☐ Unknown/Not Done

Post-Newborn Screen Molecular Test for SMN1? ☐ Yes ☐ No ☐ Unknown	What was the result? ☐ Zero copies of SMN1 (presumed homozygous deletion/conversion)* ☐ Zero copies of SMN1 (presumed homozygous deletion/conversion)* - observed on two independently collected specimens ☐ 2 pathogenic variants ☐ 2 pathogenic variants observed on two independently collected specimens ☐ 1 pathogenic variant and 1 variant of unknown significance ☐ 2 variants of unknown significance ☐ Unknown/ Not Done
Post-Newborn Screen Molecular Test for SMN2? ☐ Yes ☐ No ☐ Unknown	SMN2 Copy Number? ☐ One ☐ Two ☐ Two or more ☐ Unknown/Not Done
Parental Molecular Testing Family History/Parental Genetic Testing? ☐ Yes ☐ No ☐ Unknown	What was the result? ☐ Phasing is complete and confirms that variants are in trans or both parents are known to be carriers of the pathogenic variants identified ☐ Both parents are known carriers of SMN1 deletion ☐ Unknown/Not Done
Clinical symptoms? ☐ Present ☐ Not present ☐ Unknown	*Symptoms may include: Electromyography evidence of motor neuron disease, Absent reflexes, Fasciculations, Feeding difficulty, Hypotonia, Respiratory Difficulty, Weakness*
Was treatment started? ☐ Yes ☐ No ☐ Unknown	Type of treatment? (Check all that apply) ☐ Gene Therapy ☐ Nusinersin ☐ Other: please describe_________ ☐ Unknown

KEY: * - true deletion of exon 7 (or larger) or for which there has been a gene conversion of exon 7 (or more)