

Dataset Integrity Check for The Environmental Determinants of Diabetes in the Young (TEDDY) Clinical Trial Data Files

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1 Standard Disclaimer

The intent of this DSIC is to provide confidence that the data distributed by the NIDDK repository is a true copy of the study data. Our intent is not to assess the integrity of the statistical analyses reported by study investigators. As with all statistical analyses of complex datasets, complete replication of a set of statistical results should not be expected in secondary analysis. This occurs for a number of reasons including differences in the handling of missing data, restrictions on cases included in samples for a particular analysis, software coding used to define complex variables, etc. Experience suggests that most discrepancies can ordinarily be resolved by consultation with the study data coordinating center (DCC), however this process is labor-intensive for both DCC and Repository staff. It is thus not our policy to resolve every discrepancy that is observed in an integrity check. Specifically, we do not attempt to resolve minor or inconsequential discrepancies with published results or discrepancies that involve complex analyses, unless NIDDK Repository staff suspect that the observed discrepancy suggests that the dataset may have been corrupted in storage, transmission, or processing by repository staff. We do, however, document in footnotes to the integrity check those instances in which our secondary analyses produced results that were not fully consistent with those reported in the target publication.

2 Study Background

Since 1 September 2004 until 31 December 2010, about 350 000 newborn children were screened for high risk genotypes for type 1 diabetes in Finland, Germany, Sweden and the United States. Of these, a total of 8013 newborns were enrolled into the follow-up study. The blood samples were obtained in the maternity clinics either as cord blood or dry blood spots on day 3 to 4. [1]

Four high-risk HLA genotypes were enrolled in the Environmental determinants of Diabetes in the Young study newborn babies from the general population in Finland, Germany, Sweden and the United States. Stepwise regression analyses were used to adjust for country, parental physical characteristics and environmental factors during pregnancy. [1]

The genotype DQ4/DQ8 is associated with the lowest risk for type 1 diabetes among these four high risk genotypes. Therefore, this genotype was selected as the reference genotype in the multiple regression models and the risk estimates of the other three genotypes were based on comparison with this specific genotype. If the child was eligible for the TEDDY study based on the HLA genotype, the family was contacted by a TEDDY nurse and invited to participate in a 15-year-follow-up study. For our analysis, we included only children born as singletons, as twins and triplets are known to have lower birth weight. Children who were first-degree relatives to a subject with type 1 diabetes were excluded in this

report. Focusing on babies whose birth weight ranged from 2 to 6 kg and birth length from 40 to 60 cm, a total of 5461 children were included in the analyses. However, paternal height was only available from 1495 children. [1]

Height and weight measures in the newborn are influenced by both genetic and environmental factors. The health and nutrition status of the mother are known to influence the birth size of the baby. Women with increased blood glucose levels give birth to children with larger birth size. Retrospective epidemiological studies have indicated that young children diagnosed with type 1 diabetes were heavier or born large for gestational age. The impact of genetic factors on birth size is not fully understood. Some studies have indicated that the human leukocyte antigen (HLA) system on chromosome 6 may act on birth size. The HLA system contributes about 50% of the risk for sib-pairs to develop type 1 diabetes. The HLA genotypes conferring the highest risk in the general Caucasian population are limited to the DR3-DQA1*0501 DQB1*0201/DR4-DQA1*0301-DQB1*0302; DR4-DQA1*0301-DQB1*0302/DR4-DQA1*0301-DQB1*0302; DR8-DQA1*0401-DQB1*0402/ DR4-DQA1*0301-DQB1*0302 and DR3-DQA1*0501-DQB1*0201/ DR3-DQA1*0501-DQB1*0201 genotypes.

Results have been conflicting concerning the possible impact of these HLA-DQ genotypes on birth weight in the general population. The type 1 diabetes high-risk HLA genotypes have shown an association with higher birth weight in the general population in Sweden and Finland. Nevertheless, the same genotypes have shown a relation to lower birth weight in Norway.¹⁶ To be a carrier of any of these four genotypes was the criteria for the enrollment of newborn babies into the Environmental determinants of Diabetes in the Young (TEDDY) study. Maternal smoking influences birth size, however it is less established that the resulting reduction in birth weight may also interact with the HLA-DQ type of the child. Maternal alcohol consumption was suggested to impair intrauterine growth but results have been conflicting.¹⁹ Furthermore, parental height is related to the birth length of the baby. Taken together, it is necessary to adjust for a wide range of confounders across different populations to examine plausible effects of HLA on birth size of newborn babies in the general population. The aim of this study was, therefore, to examine the relationship between birth size and type 1 diabetes high-risk HLA genotypes in combination with prenatal characteristics in the four different countries of the multinational TEDDY study. [1]

3 Archived Datasets

All the SAS data files, as provided by the Data Coordinating Center (DCC), are located in the TEDDY folder in the data package. For this replication, variables were taken from “m8_sternery” dataset. This dataset was analysis dataset created by the DCC from the forms datasets, which are also included.

4 Statistical Methods

Analyses were performed to duplicate results for the data published by Sterner et al [1] in the Journal of Perinatology in 2011.

To verify the integrity of the dataset, descriptive statistics of baseline characteristics were computed, by genotype group (Table A, table B).

5 Results

Table 2a in the publication [1], regards the mother's height and weight at the end of pregnancy with TEDDY HLA types. Table A compares the results calculated from the archived data file to the results published in Table 2a. The results of the replication are identical to the published results.

Table 2b in the publication [1], regards the father's height with TEDDY HLA types. Table B compare the results calculated from the archived data file to the results published in Table 2a. The results of the replication are identical to the published results.

6 Conclusions

The NIDDK repository is confident that the TEDDY HLA birth size data files to be distributed are a true copy of the study data.

7 References

1. Y Sterner, C Toïrn, H-S Lee, H Larsson, C Winkler, W McLeod, K Lynch, O Simell, A Ziegler, D Schatz, W Hagopian, M Rewers, J-X She, JP Krischer, B Akolkar and A Lernmark, for the TEDDY Study Group. Country-specific birth weight and length in type 1 diabetes high-risk HLA genotypes in combination with prenatal characteristic. Journal of Perinatology. 2011; 0743-8346/11

Table A: Comparison of values computed in integrity check to reference article Table 2a values: Mother height and weight at the end of pregnancy with TEDDY HLA types

Mother Height

	N [Manuscript]	N [DSIC]	N [Difference]	Pr>F [Manuscript]	Pr>F [DSIC]	Pr>F [Difference]
Over All	5328	5328	0	0.001	0.001	0
United States	2023	2023	0	0.012	0.012	0
Finland	1128	1128	0	0.999	0.999	0
Germany	275	275	0	0.131	0.131	0
Sweden	1902	1902	0	0.228	0.228	0

	TEDDY HLA genotype	PE [Manuscript]	PE [DSIC]	PE [Difference]	s.e. [Manuscript]	s.e. [DSIC]	s.e. [Difference]	Pr> t [Manuscript]	Pr> t [DSIC]	Pr> t [Difference]
OverAll	AvsC	0.68	0.68	0	0.264	0.264	0	0.01	0.01	0
	BvsC	0.446	0.446	0	0.302	0.302	0	0.14	0.14	0
	DvsC	1.14	1.14	0	0.298	0.298	0	<.0001	0	0
United States	AvsC	1.056	1.056	0	0.514	0.514	0	0.04	0.04	0
	BvsC	1.059	1.059	0	0.576	0.576	0	0.066	0.066	0
	DvsC	1.846	1.846	0	0.558	0.558	0	0.001	0.001	0
Finland	AvsC	-0.018	-0.018	0	0.435	0.435	0	0.966	0.967	0
	BvsC	0.064	0.064	0	0.544	0.544	0	0.906	0.906	0
	DvsC	0.017	0.017	0	0.555	0.555	0	0.975	0.975	0
Germany	AvsC	0.904	0.904	0	1.252	1.252	0	0.471	0.471	0
	BvsC	0.943	0.943	0	1.42	1.42	0	0.507	0.507	0
	DvsC	2.7	2.7	0	1.346	1.346	0	0.046	0.046	0
Sweden	AvsC	0.273	0.273	0	0.445	0.445	0	0.539	0.539	0
	BvsC	-0.372	-0.372	0	0.492	0.492	0	0.45	0.45	0
	DvsC	0.44	0.44	0	0.493	0.493	0	0.372	0.372	0

Mother weight at the end of pregnancy

	N [Manuscript]	N [DSIC]	Pr>F [Manuscript]	Pr>F [DSIC]	Pr>F [Difference]
OverAll	5255	5255	<.0001	<.0001	0
United States	2007	2007	0.042	0.042	0
Finland	1122	1122	0.543	0.544	0
Germany	274	274	0.216	0.216	0
Sweden	1852	1852	0.017	0.017	0

	TEDDY HLA genotype	PE [Manuscript]	PE [DSIC]	PE [Difference]	s.e. [Manuscript]	s.e. [DSIC]	s.e. [Difference]	Pr> t [Manuscript]	Pr> t [DSIC]	Pr> t [Difference]
OverAll	AvsC	1.13	1.13	0	0.578	0.578	0	0.051	0.051	0
	BvsC	0.853	0.853	0	0.662	0.662	0	0.198	0.198	0
	DvsC	3.145	3.145	0	0.652	0.652	0	<.0001	<.0001	0
United States	AvsC	1.644	1.644	0	1.134	1.134	0	0.147	0.148	0
	BvsC	0.844	0.844	0	1.274	1.274	0	0.508	0.508	0
	DvsC	3.246	3.246	0	1.234	1.234	0	0.009	0.009	0
Finland	AvsC	0.148	0.148	0	0.892	0.892	0	0.869	0.869	0
	BvsC	-0.297	-0.297	0	1.116	1.116	0	0.79	0.79	0
	DvsC	1.452	1.452	0	1.138	1.138	0	0.202	0.202	0
Germany	AvsC	4.153	4.153	0	2.979	2.979	0	0.164	0.164	0
	BvsC	5.397	5.397	0	3.376	3.376	0	0.111	0.111	0
	DvsC	6.576	6.576	0	3.201	3.201	0	0.041	0.041	0
Sweden	AvsC	-2.026	-2.026	0	0.99	0.99	0	0.041	0.041	0
	BvsC	-2.033	-2.033	0	1.093	1.093	0	0.063	0.063	0
	DvsC	0.15	0.15	0	1.098	1.098	0	0.892	0.892	0

Table B: Comparison of values computed in integrity check to reference article Table 2b values: Father height with TEDDY HLA types

	N [Manuscript]	N [DSIC]	N [Difference]	Pr>F [Manuscript]	Pr>F [DSIC]	Pr>F [Difference]
OverAll	1495	1495	0	0.015	0.015	0
United States	513	513	0	0.073	0.073	0
Finland	235	235	0	0.588	0.588	0
Germany	87	87	0	0.763	0.764	0
Sweden	660	660	0	0.447	0.448	0

	TEDDY HLA genotype	PE [Manuscript]	PE [DSIC]	PE [Difference]	s.e. [Manuscript]	s.e. [DSIC]	s.e. [Difference]	Pr> t [Manuscript]	Pr> t [DSIC]	Pr> t [Difference]
OverAll	AvsC	0.864	0.864	0	0.537	0.537	0	0.108	0.108	0
	BvsC	0.292	0.292	0	0.614	0.614	0	0.634	0.634	0
	DvsC	1.771	1.771	0	0.602	0.602	0	0.003	0.003	0
United States	AvsC	1.438	1.438	0	1.045	1.045	0	0.169	0.17	0
	BvsC	0.705	0.705	0	1.158	1.158	0	0.543	0.543	0
	DvsC	2.74	2.74	0	1.127	1.127	0	0.015	0.015	0
Finland	AvsC	-0.501	-0.501	0	1.196	1.196	0	0.676	0.676	0
	BvsC	-1.095	-1.095	0	1.439	1.439	0	0.448	0.448	0
	DvsC	1.204	1.204	0	1.535	1.535	0	0.433	0.434	0
Germany	AvsC	-0.664	-0.664	0	2.233	2.233	0	0.767	0.767	0
	BvsC	1.314	1.314	0	2.645	2.645	0	0.621	0.621	0
	DvsC	0.952	0.952	0	2.456	2.456	0	0.699	0.699	0
Sweden	AvsC	0.906	0.906	0	0.806	0.806	0	0.261	0.261	0
	BvsC	0.307	0.307	0	0.911	0.911	0	0.736	0.736	0
	DvsC	1.252	1.252	0	0.896	0.896	0	0.163	0.163	0

Attachment A: SAS Code

```

/*****
***Program: /prj/niddk/ims_analysis/TEDDY/prog_initial_analysis/teddy_integrity_check.sas;
***Programmer: Jane
***Date Created: 12/10/2013
***Purpose: To perform a Dataset Integrity Check (DSIC) between the TEDDY data and the primary outcome paper:
*** Y Sterner, C Torn, H-S Lee, H Larsson, C Winkler, W McLeod, K Lynch, O Simell, A Ziegler, D Schatz, W Hagopian, M Rewers,
*** J-X She, JP Krischer, B Akolkar and A Lernmark, for the TEDDY Study Group. Country-specific birth weight and length in
*** type 1 diabetes high-risk HLA genotypes in combination with prenatal characteristic.
*** Journal of Perinatology. 2011; 0743-8346/11
*** The numbers in Tables 2a, and 2b of the primary outcome paper will compared to the TEDDY data received;
*****/

title1 "%sysfunc(getoption(sysin))";

title2 " ";

options nofmterr;

libname sas_data "/prj/niddk/ims_analysis/TEDDY/private_orig_data/new/";

proc format;

value hlargc 1='DR3/4' 2='DR4/4' 4='DR4/8' 9='DR3/3';

*** Reading in the analysis datasets used for the DSIC;

data m8_sternery      ;

    set sas_data.m8_sternery      ;

*** Data from the Primary outcome paper that was converted to .csv format so that the DSIC data could be easily compared;

FILENAME table2a1  '/prj/niddk/ims_analysis/TEDDY/private_created_data/table2a_data_motherheight.csv';

FILENAME table2a2  '/prj/niddk/ims_analysis/TEDDY/private_created_data/table2a_data_motherweight.csv';

FILENAME table2b   '/prj/niddk/ims_analysis/TEDDY/private_created_data/table2b_data_fatherheight.csv';
```

```

*** Output CSV files that will be converted to .xls before being added to the DSIC document;
FILENAME out_t2a1  '/prj/niddk/ims_analysis/TEDDY/private_created_data/teddy_table2a_mht_dsic.csv';
FILENAME out_t2a2  '/prj/niddk/ims_analysis/TEDDY/private_created_data/teddy_table2a_mwt_dsic.csv';
FILENAME out_t2b   '/prj/niddk/ims_analysis/TEDDY/private_created_data/teddy_table2b_fht_dsic.csv';

proc sort data = m8_sternery; by country; run;

%macro baseline_GLM(var_name);
    *** Creating a statistical analyses in the format of Table 2 in the primary outcome paper;
    proc glm data = m8_sternery;
        class hlarg;
        model &var_name=hlarg /ss3 solution clparm;
        lsmean hlarg/ stderr pdiff adjust=tukey;
    *** Outputting the statistics to dataset using the ODS output;
        ods output ModelANOVA = &var_name.pr_f  ParameterEstimates = &var_name.glm ;
    *** Creating a statistical analyses in the format of Table 2 in the primary outcome paper;
    proc glm data = m8_sternery;
        class hlarg;
        model &var_name=hlarg /ss3 solution clparm;
        lsmean hlarg/ stderr pdiff adjust=tukey;
        by country;
    *** Outputting the statistics to dataset using the ODS output;
        ods output ModelANOVA = &var_name.pr_f_bycontry  ParameterEstimates = &var_name.glm_bycontry ;

```

```

*** Creating a frequency table in the format of Table 2 in the primary outcome paper;

proc freq data = m8_sternery ;

    tables COUNTRY ;

    where not missing(&var_name) ;

ods output OneWayFreqs = work.&var_name.COUNT_bycontry;

data &var_name.COUNT(keep = COUNTRY    CumFrequency);

    set &var_name.COUNT_bycontry;

    if COUNTRY = 4;

    COUNTRY = 0;

*** Creating two datasets (one per arm) so that the data can be in the correct format;

data &var_name.COUNT_all(keep = COUNTRY    Frequency);

    set &var_name.COUNT(rename = ( CumFrequency=Frequency)) &var_name.COUNT_bycontry;

data &var_name.pr_f_all(keep =COUNTRY ProbF );

    set &var_name.pr_f &var_name.pr_f_bycontry;

    if missing(COUNTRY) then COUNTRY = 0;

    ProbF    = round(ProbF,0.001);

data &var_name.COUNT_pf;

    merge &var_name.COUNT_all    &var_name.pr_f_all;

    by COUNTRY;

data &var_name.glm_all(keep = COUNTRY    Parameter    Estimate    StdErr    Probt );

    set &var_name.glm &var_name.glm_bycontry;

    if Parameter ne 'Intercept';

```

```

if not missing(StdErr);

if missing(COUNTRY) then COUNTRY = 0;

Parameter = compress(substr(Parameter,11,5));

Estimate = round(Estimate,0.001);

StdErr = round(StdErr,0.001);

Probt = round(Probt,0.001);

%mend;

%baseline_GLM(fatherheight );

%baseline_GLM(CMOMHEIGHT );

%baseline_GLM(MOMWEIGHT_END );

*** Importing the Table 2a mother weight Data taken from the primary outcome paper;

*** Please note import error_message mother weight, need to modify output .csv file of ProbF is <0.0001 ProbT is <0.0001 part;

data table2a2_data;

infile table2a2 delimiter = ',' MISSOVER DSD firstobs=3 ls=1080;

length Parameter $16.;

input COUNTRY          Parameter $ n          Estimate          StdErr Probt ProbF error_message $

;

data table2a2_count(keep = COUNTRY n ProbF rename = (ProbF=ProbF_table n= Frequency_table) )

table2a2_glm(keep = COUNTRY sort_order Parameter Estimate StdErr Probt

rename =( Estimate=Estimate_table StdErr=StdErr_table Probt=Probt_table));

```

```

set table2a2_data;

sort_order = _n_;

Parameter = compress (Parameter);

if n ne . then output table2a2_count;

output table2a2_glm;

*** Importing the Table 2a mother height Data taken from the primary outcome paper;

data table2a1_data;

infile table2a1 delimiter = ',' MISSOVER DSD firstobs=3 ls=1080;

length Parameter $16.;

input COUNTRY      Parameter $   n      Estimate      StdErr Probt   ProbF e $
;

data table2a1_count(keep = COUNTRY   n   ProbF rename = (ProbF=ProbF_table n= Frequency_table) )
    table2a1_glm(keep = COUNTRY sort_order Parameter Estimate StdErr Probt
        rename =( Estimate=Estimate_table StdErr=StdErr_table Probt=Probt_table));

set table2a1_data;

sort_order = _n_;

Parameter = compress (Parameter);

if n ne . then output table2a1_count;

output table2a1_glm;

*** Importing the Table 2b father height Data taken from the primary outcome paper;

```

```

data table2b_data;

  infile table2b delimiter = ',' MISSOVER DSD firstobs=3 ls=1080;

  length Parameter $16.;

  input COUNTRY      Parameter $   n      Estimate      StdErr  Probt  ProbF e $
;

data table2b_count(keep = COUNTRY   n   ProbF rename = (ProbF=ProbF_table n= Frequency_table) )

  table2b_glm(keep = COUNTRY sort_order Parameter Estimate StdErr Probt

              rename =( Estimate=Estimate_table StdErr=StdErr_table Probt=Probt_table));

set table2b_data;

sort_order = _n_;

Parameter = compress (Parameter);

if n ne . then output  table2b_count;

output table2b_glm;

%macro compare_GLM(table_name, var_name);

proc sort data = &table_name._glm;

  by COUNTRY Parameter;

proc sort data = &var_name.glm_all;

  by COUNTRY Parameter;

data &var_name._glmcombine prob;

  merge &var_name.glm_all(in = in1) &table_name._glm(in = in2);

```

```

    by COUNTRY Parameter;

    if in1 and in2 then output &var_name._glmcombine;

    else output prob;

data &var_name._glmcombine;

    set &var_name._glmcombine;

    diff_Estimate = round((Estimate-Estimate_table),1);

    diff_StdErr   = round((StdErr -StdErr_table),1);

    diff_Probt    = round((Probt -Probt_table),1);

proc sort data = &table_name._count;

    by COUNTRY ;

proc sort data = &var_name.COUNT_pf;

    by COUNTRY ;

data &var_name._countcombine prob;

    merge &var_name.COUNT_pf(in = in1) &table_name._count(in = in2);

    by COUNTRY ;

    if in1 and in2 then output &var_name._countcombine;

    else output prob;

data &var_name._countcombine;

    set &var_name._countcombine;

    diff_ProbF = round((ProbF-ProbF_table),1);

    diff_Frequency = round((Frequency -Frequency_table),1);

%mend;

```



```

%compare_GLM(table2b, fatherheight );
%compare_GLM(table2a1, CMOMHEIGHT );
%compare_GLM(table2a2, MOMWEIGHT_END );

data table2a1_motherheight_out;

  set CMOMHEIGHT_countcombine CMOMHEIGHT_glmcombine;

  label

  country          = "country"

  Parameter        = "TEDDY HLA genotype"

  Frequency        = "N [Manuscript]"

  Frequency_table  = "N [DSIC]      "

  diff_Frequency   = "N [Difference]"

  Estimate         = "PE [Manuscript]"

  Estimate_table   = "PE [DSIC]      "

  diff_Estimate    = "PE [Difference]"

  StdErr          = "s.e. [Manuscript]"

  StdErr_table     = "s.e. [DSIC]      "

  diff_StdErr      = "s.e. [Difference]"

  Probt           = "Pr>|t| [Manuscript]"

  Probt_table      = "Pr>|t| [DSIC]      "

  diff_Probt       = "Pr>|t| [Difference]"

  ProbF           = "Pr>F [Manuscript]"

```

```

ProbF_table      = "Pr>F [DSIC]      "
diff_ProbF      = "Pr>F [Difference]"
;
proc sort data = table2a1_motherheight_out;

  by country sort_order;

data table2a2_motherweight_out;

  set MOMWEIGHT_END_countcombine MOMWEIGHT_END_glmcombine;

  label

  country        = "country"

  Parameter      = "TEDDY HLA genotype"

  Frequency      = "N [Manuscript]"

  Frequency_table = "N [DSIC]      "

  diff_Frequency = "N [Difference]"

  Estimate       = "PE [Manuscript]"

  Estimate_table = "PE [DSIC]      "

  diff_Estimate  = "PE [Difference]"

  StdErr        = "s.e. [Manuscript]"

  StdErr_table  = "s.e. [DSIC]      "

  diff_StdErr   = "s.e. [Difference]"

  Probt         = "Pr>|t| [Manuscript]"

  Probt_table   = "Pr>|t| [DSIC]      "

  diff_Probt    = "Pr>|t| [Difference]"

```

```

ProbF          = "Pr>F [Manuscript]"
ProbF_table    = "Pr>F [DSIC]      "
diff_ProbF     = "Pr>F [Difference]"
;
proc sort data = table2a2_motherweight_out;
  by country sort_order;
data table2b_fatherheight_out;
  set fatherheight_countcombine fatherheight_glmcombine;
  label
country          = "country"
Parameter        = "TEDDY HLA genotype"
Frequency        = "N [Manuscript]"
Frequency_table  = "N [DSIC]      "
diff_Frequency   = "N [Difference]"
Estimate         = "PE [Manuscript]"
Estimate_table   = "PE [DSIC]      "
diff_Estimate    = "PE [Difference]"
StdErr          = "s.e. [Manuscript]"
StdErr_table     = "s.e. [DSIC]      "
diff_StdErr      = "s.e. [Difference]"
Probt           = "Pr>|t| [Manuscript]"
Probt_table      = "Pr>|t| [DSIC]      "
diff_Probt       = "Pr>|t| [Difference]"

```

```
ProbF          = "Pr>F [Manuscript]"
ProbF_table    = "Pr>F [DSIC]      "
diff_ProbF     = "Pr>F [Difference]"
;

proc sort data = table2b_fatherheight_out;
  by country sort_order;
*** Outputting the data to a csv format to be added to the DSIC;
ods csv file = out_t2a1;
run;

proc print data = table2a1_motherheight_out NOOBS label; var
country
Parameter
Frequency
Frequency_table
diff_Frequency
Estimate
Estimate_table
diff_Estimate
StdErr
StdErr_table
diff_StdErr
Probt
```

```
Probt_table
diff_Probt
ProbF
ProbF_table
diff_ProbF
;
      title "DSIC Check of Table 2a (mother height): Mother height and weight at the end of pregnancy with TEDDY HLA types";
run;

*** Outputting the data to a csv format to be added to the DSIC;
ods csv file = out_t2a2;
run;

proc print data = table2a2_motherweight_out NOOBS label;var
country
Parameter
Frequency
Frequency_table
diff_Frequency
Estimate
Estimate_table
diff_Estimate
```

```
StdErr
```

```
StdErr_table
```

```
diff_StdErr
```

```
Probt
```

```
Probt_table
```

```
diff_Probt
```

```
ProbF
```

```
ProbF_table
```

```
diff_ProbF
```

```
;
```

```
title "DSIC Check of Table 2a (mother weight): Mother height and weight at the end of pregnancy with TEDDY HLA types";
```

```
run;
```

```
*** Outputting the data to a csv format to be added to the DSIC;
```

```
ods csv file = out_t2b;
```

```
run;
```

```
proc print data = table2b_fatherheight_out NOOBS label;var
```

```
country
```

```
Parameter
```

```
Frequency
```

```
Frequency_table
```

```
diff_Frequency
Estimate
Estimate_table
diff_Estimate
StdErr
StdErr_table
diff_StdErr
Probt
Probt_table
diff_Probt
ProbF
ProbF_table
diff_ProbF
;
    title "DSIC Check of Table 2b (father weight): Father height with TEDDY HLA types";
run;
```