

Dataset Integrity Check for The Environmental Determinants of Diabetes in the Young (TEDDY) Pub81 Lonnot

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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

The TEDDY study was designed to follow children with and without a family history of T1D to understand the environmental factors that contribute to the disease. Newborn children younger than 4 months were screened for high-risk HLA alleles, and those with qualifying haplotypes were eligible for follow-up. Information is collected on medical information (infections, medication, immunizations), exposure to dietary and other environmental factors, negative life events, family history, tap water, and measurements of psychological stress. Biospecimens, including blood, stool, urine, and nail clippings, are taken at baseline and follow-up study visits. The primary outcome measures include two endpoints—the first appearance of one or more islet cell autoantibodies (GADA, IAA, or IA-2A), confirmed at two consecutive visits, and development of T1D. The cohort will be followed for 15 years, or until the occurrence of one of the primary endpoints.

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 the “m_81_lonnrot_niddk_31dec2012_1.sas7bdat”, “m_81_lonnrot_niddk_31dec2012_2.sas7bdat”, and “m_81_lonnrot_niddk_31dec2012_3.sas7bdat” datasets.

4 Statistical Methods

Analyses were performed to duplicate results for the data published by Lonrot et al [1] in BMC Pediatrics in 2015. To verify the integrity of the dataset, descriptive statistics were computed.

5 Results

For Table 1 in the publication [1], Categories of infections arranged into four infectious episode types, Table A lists the variables that were used in the replication and Table B compares the results calculated from the archived data files to the results published in Table 1. The results of the replication are an exact match to the published results.

For Figure 2 in the publication [1], Infectious episode rates by season, Table C lists the variables that were used in the replication and Figure A compares the results calculated from the archived data files to the results published in Figure 2. The results of the replication are almost an exact match to the published results.

For Figure 3 in the publication [1], Infectious episode rates by age, Table D lists the variables that were used in the replication and Figure B compares the results calculated from the archived data files to the results published in Figure 3. The results of the replication are an exact match to published results.

For Table 2 in the publication [1], Infectious episode rates by subject attributes, Table E lists the variables that were used in the replication and Table F compares the results calculated from the archived data files to the results published in Table 2. The results of the publication are almost an exact match to published results.

6 Conclusions

The NIDDK repository is confident that the TEDDY M81 data files to be distributed are a true copy of the study data.

7 References

[1] Lonnrot, M., Lynch, K., Larsson, H.E., Lernmark, A., Rewers, M., Hagopian, W., She, J., Simell, O., Ziegler, A., Akolkar, B., Krischer, J., Hyoty, H., and the TEDDY study group. "A method for reporting and classifying acute infectious disease in a prospective study of young children: TEDDY". BMC Pediatrics (2015) 15:24.

Table A: Variables used to replicate Table 1: Categories of infections arranged into four infectious episode types

Table Variable	dataset.variable
Infectious episode type	m_81_lonnrot_niddk_31dec2012_2.inf_epi_group
Febrile infectious episode	m_81_lonnrot_niddk_31dec2012_2.fever_yes

Table B: Comparison of values computed in integrity check to reference article Table 1 values

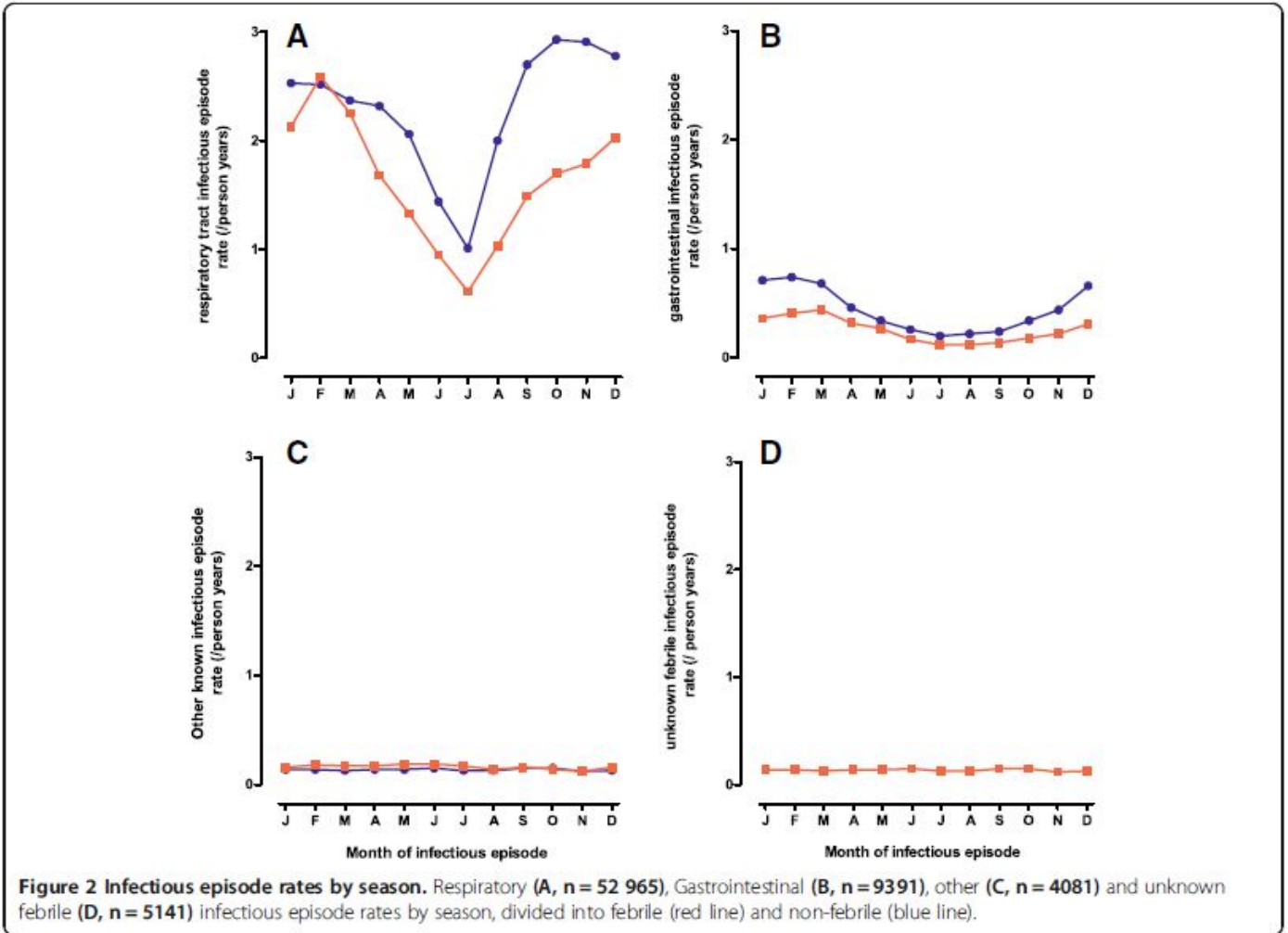
Infectious episode type	Number of infectious episodes (% of total 71578) Manuscript	Number of infectious episodes (% of total 71578) DSIC	Diff. (n = 0)	Percent of febrile infectious episodes Manuscript	Percent of febrile infectious episodes DSIC	Diff.
Respiratory	52965 (74.0)	52965 (74.0)	0 (0)	41.5	41.5	0
Gastrointestinal	9391 (13.1)	9391 (13.1)	0 (0)	36.6	36.6	0
Other	4081 (5.7)	4081 (5.7)	0 (0)	54	54.0	0
Unknown febrile	5141 (7.2)	5141 (7.2)	0 (0)	100	100	0

Table C: Variables used to replicate Figure 2: Infectious episode rates by season

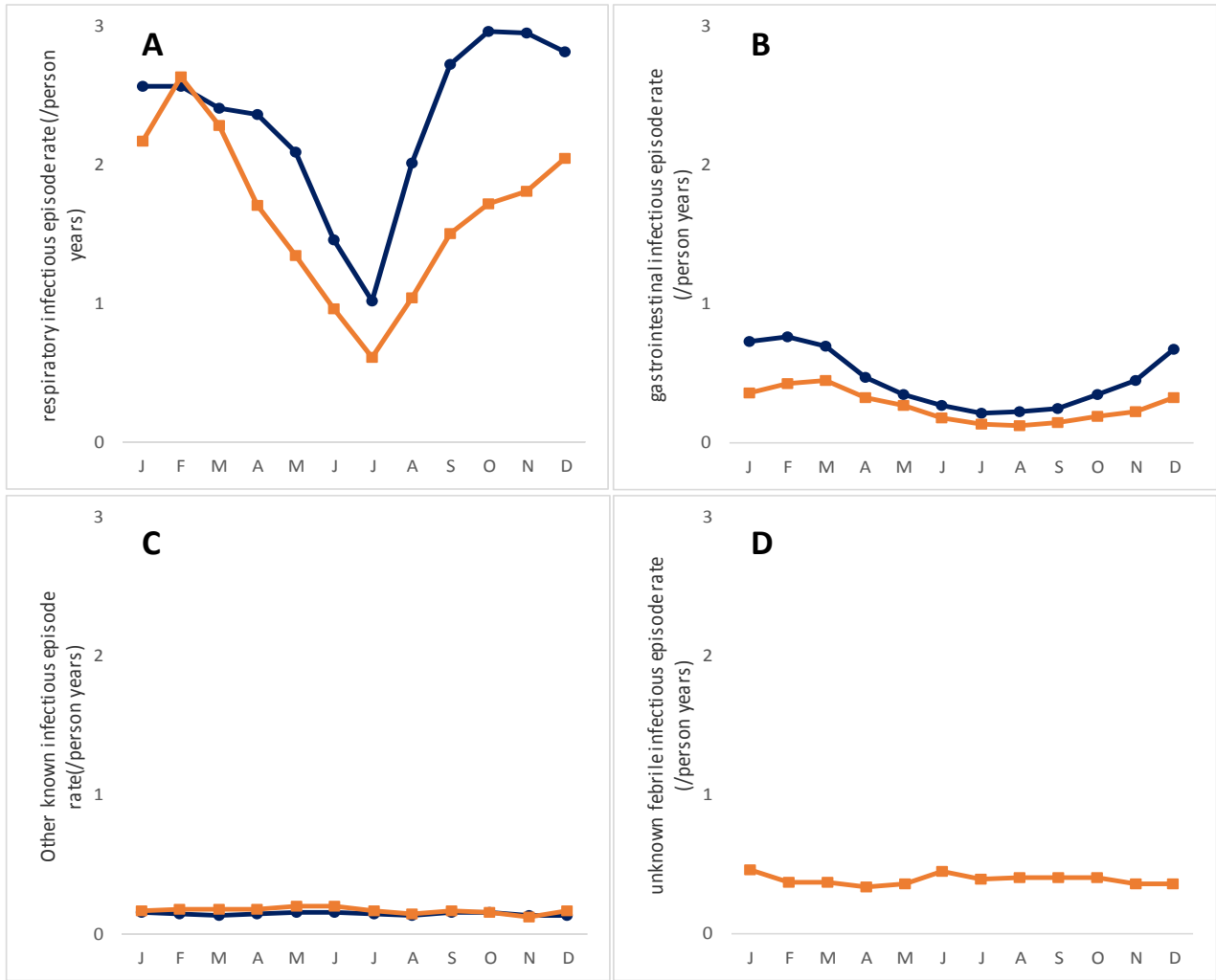
Chart Variable	dataset.variable
Infectious episode type	m_81_lonnrot_niddk_31dec2012_2.inf_epi_group
Febrile infectious episode	m_81_lonnrot_niddk_31dec2012_2.fever_yes
Month	m_81_lonnrot_niddk_31dec2012_2.month_inf_reported
Person years	m_81_lonnrot_niddk_31dec2012_2.age_days_episode

Figure A: Comparison of values computed in integrity check to reference article Figure 2 values

Manuscript:



DSIC



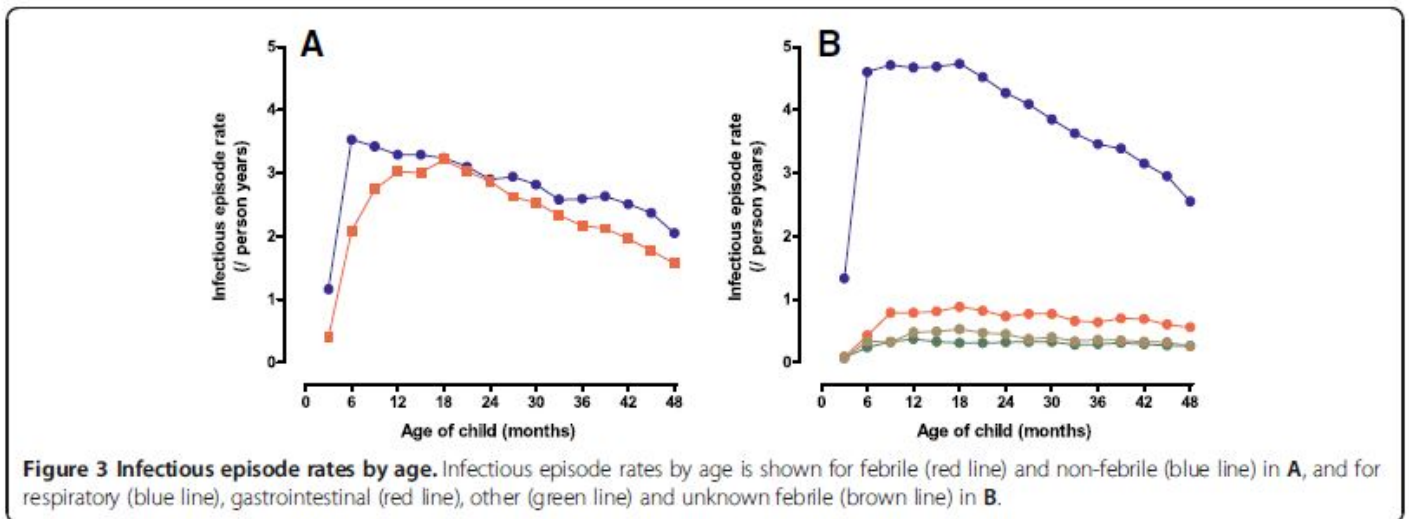
Infectious episode rates by season. Respiratory (A, n=52 965), Gastrointestinal (B, n=9391), other (C, n=4081), and unknown febrile (D, n=5141) infectious episode rates by season, divided into febrile (red line) and non-febrile (blue line).

Table D: Variables used to replicate Figure 3: Infectious episode rates by age

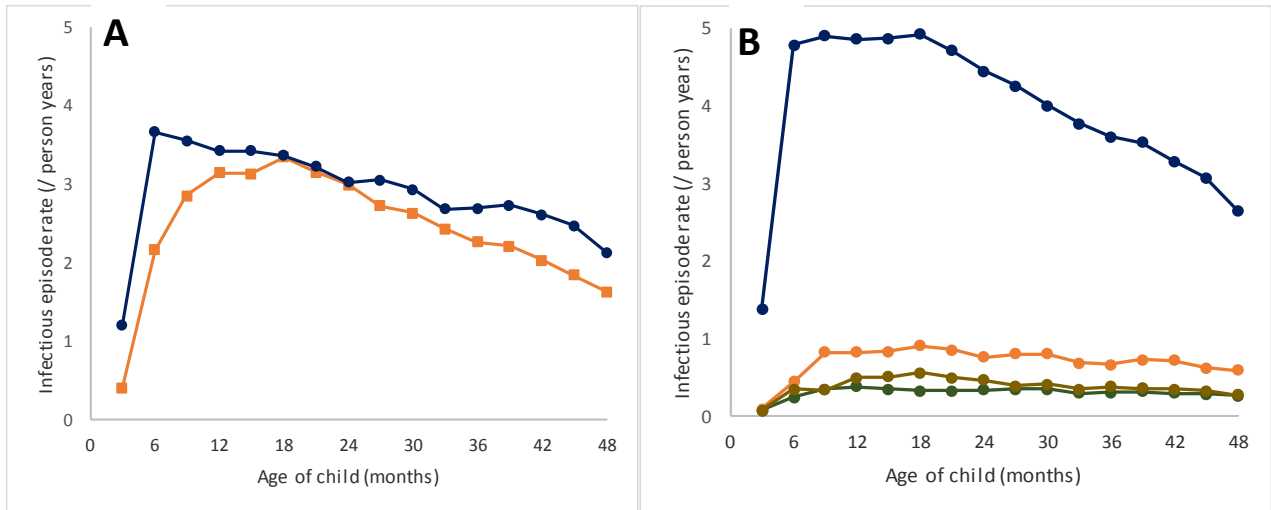
Chart Variable	dataset.variable
Febrile infectious episodes	m_81_lonnrot_niddk_31dec2012_3.sum_inf_fever
Non-febrile infectious episodes	m_81_lonnrot_niddk_31dec2012_3.sum_inf_no_fever
Respiratory infectious episodes	m_81_lonnrot_niddk_31dec2012_3.sum_respir_all
Gastrointestinal infectious episodes	m_81_lonnrot_niddk_31dec2012_3.sum_gastro_all
Other infectious episodes	m_81_lonnrot_niddk_31dec2012_3.sum_ICD_all
Unknown febrile infectious episodes	m_81_lonnrot_niddk_31dec2012_3.sum_fever_only_all
Age	m_81_lonnrot_niddk_31dec2012_3.visit
Person years	m_81_lonnrot_niddk_31dec2012_2.age_days_episode

Figure B: Comparison of values computed in integrity check to reference article Figure 3 values

Manuscript



DSIC



Infectious episode rates by age. Infectious episode rates by age is shown for febrile (red line) and non-febrile (blue line) in **A**, and for respiratory (blue line), gastrointestinal (red line), other (green line), and unknown febrile (brown line) in **B**.

Table E: Variables used to replicate Table 2: Infectious episode rates by subject attributes

Table Variable	dataset.variable
Any infectious episode	m_81_lonnrot_niddk_31dec2012_3.sum_inf_all
Febrile infectious episodes	m_81_lonnrot_niddk_31dec2012_3.sum_inf_fever
Non-febrile infectious episodes	m_81_lonnrot_niddk_31dec2012_3.sum_inf_no_fever
Site	m_81_lonnrot_niddk_31dec2012_3.cc
Gender of child	m_81_lonnrot_niddk_31dec2012_3.female
First degree relative with T1D	m_81_lonnrot_niddk_31dec2012_3.fdr
HLA-DR-DQ genotype	m_81_lonnrot_niddk_31dec2012_3.hla_5grps

Table F: Comparison of values computed in integrity check to reference article Table 2 values

Factor	Any infectious episode rate ratios (RR)					
	RR Manuscript	RR DSIC	Diff.	95% CI Manuscript	95% CI DSIC	Diff.
Site						
Colorado	1.00	1.00	0	ref	ref	N/A
Georgia	1.18	1.18	0	1.14-1.22	1.14-1.21	0-0.01
Washington	1.05	1.05	0	1.02-1.09	1.02-1.08	0-0.01
Finland	1.50	1.50	0	1.46-1.54	1.48-1.53	0.02-0.01
Germany	1.40	1.40	0	1.34-1.45	1.35-1.44	0.01-0.01
Sweden	1.42	1.42	0	1.39-1.46	1.40-1.45	0.01-0.01
Gender of child						
Female	1.00	1.00	0	ref	ref	N/A
Male	1.04	1.04	0	1.02-1.05	1.02-1.05	0-0
First degree relative with T1D						
No	1.00	1.00	0	ref	ref	N/A
Yes	1.01	1.01	0	0.98-1.04	0.99-1.04	0.01-0
HLA-DR-DQ genotype						
DR4/DR4	1.00	1.00	0	ref	ref	N/A
DR3/DR4	1.02	1.02	0	1.00-1.04	1.01-1.04	0.01-0
DR4/DR8	0.97	0.97	0	0.94-0.99	0.94-0.99	0-0
DR3/DR3	0.99	0.99	0	0.97-1.01	0.97-1.01	0-0
HLA-specific	0.98	0.98	0	0.93-1.03	0.94-1.02	0.01-0.01

Factor	Febrile infectious episode rate ratios (RR)					
	RR Manuscript	RR DSIC	Diff.	95% CI Manuscript	95% CI DSIC	Diff.
Site						
Colorado	1.00	1.00	0	ref	ref	N/A
Georgia	1.30	1.30	0	1.23-1.37	1.24-1.36	0.01-0.01
Washington	1.03	1.03	0	0.97-1.09	0.98-1.08	0.01-0.01
Finland	1.95	1.95	0	1.87-2.04	1.90-2.00	0.03-0.04
Germany	1.80	1.80	0	1.69-1.92	1.71-1.90	0.02-0.02
Sweden	2.39	2.39	0	2.30-2.49	2.34-2.45	0.04-0.04

Factor	Febrile infectious episode rate ratios (RR)					
	RR Manuscript	RR DSIC	Diff.	95% CI Manuscript	95% CI DSIC	Diff.
Gender of child						
Female	1.00	1.00	0	ref	ref	N/A
Male	1.03	1.03	0	1.00-1.05	1.00-1.05	0-0
First degree relative with T1D						
No	1.00	1.00	0	ref	ref	N/A
Yes	0.97	0.97	0	0.93-1.01	0.94-1.01	0.01-0
HLA-DR-DQ genotype						
DR4/DR4	1.00	1.00	0	ref	ref	N/A
DR3/DR4	0.99	0.99	0	0.96-1.02	0.96-1.01	0-0.01
DR4/DR8	0.97	0.97	0	0.93-1.01	0.94-1.00	0.01-0.01
DR3/DR3	0.92	0.92	0	0.89-0.95	0.89-0.95	0-0
HLA-specific	1.01	1.01	0	0.94-1.09	0.95-1.08	0.01-0.01

Factor	Non-febrile infectious episode rate ratios (RR)					
	RR Manuscript	RR DSIC	Diff.	95% CI Manuscript	95% CI DSIC	Diff.
Site						
Colorado	1.00	1.00	0	ref	ref	N/A
Georgia	1.12	1.12	0	1.07-1.16	1.08-1.16	0.01-0
Washington	1.06	1.06	0	1.02-1.10	1.02-1.09	0-0.01
Finland	1.28	1.28	0	1.24-1.32	1.25-1.31	0.01-0.01
Germany	1.19	1.19	0	1.13-1.25	1.14-1.25	0.01-0
Sweden	0.94	0.94	0	0.91-0.97	0.92-0.96	0.01-0.01
Gender of child						
Female	1.00	1.00	0	ref	ref	N/A
Male	1.05	1.05	0	1.03-1.07	1.03-1.07	0-0
First degree relative with T1D						
No	1.00	1.00	0	ref	ref	N/A
Yes	1.05	1.04	0.01	1.01-1.09	1.01-1.08	0-0.01
HLA-DR-DQ genotype						
DR4/DR4	1.00	1.00	0	ref	ref	N/A
DR3/DR4	1.05	1.05	0	1.02-1.08	1.03-1.08	0.01-0

Factor	Non-febrile infectious episode rate ratios (RR)					
	RR Manuscript	RR DSIC	Diff.	95% CI Manuscript	95% CI DSIC	Diff.
DR4/DR8	0.96	0.96	0	0.93-1.00	0.93-0.99	0-0.01
DR3/DR3	1.05	1.05	0	1.02-1.09	1.02-1.08	0-0.01
HLA-specific	0.95	0.96	0.01	0.89-1.02	0.90-1.01	0.01-0.01

Attachment A: SAS Code

```
**** TEDDY M81 DSIC;
****
**** Programmer: Allyson Mateja;
**** Date: August 9, 2016;

title '/prj/niddk/ims_analysis/TEDDY/prog_initial_analysis/teddy_integrity_check_m81.sas';
title2 ' ';

proc format;
    value groupf 1 = 'Respiratory'
                2 = 'Gastrointestinal'
                3 = 'Other'
                4 = 'Unknown febrile';

    value yesnof 0 = 'No'
                 1 = 'Yes';

    value ccf 1 = 'US-Colorado'
              2 = 'US-Georgia'
              3 = 'US-Washington'
              4 = 'Europe-Finland'
              5 = 'Europe-Germany'
              6 = 'Europe-Sweden';

    value hlaf 1 = 'DR3/4'
               2 = 'DR4/4'
               3 = 'DR4/8'
               4 = 'FDR specific'
               5 = 'DR3/3';

libname privorig '/prj/niddk/ims_analysis/TEDDY/private_orig_data/M_81_MLonnrot_NIDDK_Submission/';

data m81_data_part1;
    set privorig.m_81_mlonnrot_niddk_31dec2012_1;

proc contents data = m81_data_part1;

data m81_data_part2;
    set privorig.m_81_mlonnrot_niddk_31dec2012_2;

proc contents data = m81_data_part2;

data m81_data_part3;
    set privorig.m_81_mlonnrot_niddk_31dec2012_3;

proc contents data = m81_data_part3;
```

```

proc freq data = m81_data_part2;
  tables inf_epi_group;
  format inf_epi_group groupf.;
  title3 'Table 1 - Number of Infectious episodes';

proc sort data = m81_data_part2;
  by inf_epi_group;

proc freq data = m81_data_part2;
  tables fever_yes;
  by inf_epi_group;
  format inf_epi_group groupf. fever_yes yesnof.;
  title3 'Table 1 - Percent of febrile infectious episodes';

*** Figure 2 - Use calculated 'infectious_rate' variable to create graphs in Excel;

data m81_data_part2;
  set m81_data_part2;
  age_years_episode = age_days_episode/365.25;

proc sort data = m81_data_part2;
  by maskid age_years_episode;

data last_infection;
  set m81_data_part2;
  by maskid;
  if last.maskid then output;

proc means data = last_infection n sum;
  var age_years_episode;
  output out = mean_data sum=sum;
  title3 'Total Person Years';

data mean_data;
  set mean_data;
  person_years = sum/12;
  merge_flag = 1;

proc freq data = m81_data_part2;
  tables month_inf_reported /out = freq_data;
  where inf_epi_group = 1 and fever_yes = 0 ;
  title3 'Figure 2 - Non-Febrile Respiratory Infectious episode rate';

data freq_data;
  set freq_data;
  merge_flag = 1;

data person_year_data;
  merge freq_data
        mean_data;
  by merge_flag;

```

```

        infectious_rate = (count/person_years);

proc print data = person_year_data;

proc freq data = m81_data_part2;
    tables month_inf_reported /out = freq_data;
    where inf_epi_group = 1 and fever_yes = 1;
    title3 'Figure 2 - Febrile Respiratory Infectious episode rate';

data freq_data;
    set freq_data;
    merge_flag = 1;

data person_year_data;
    merge freq_data
          mean_data;
    by merge_flag;
    infectious_rate = (count/person_years);

proc print data = person_year_data;

proc freq data = m81_data_part2;
    tables month_inf_reported /out = freq_data;
    where inf_epi_group = 2 and fever_yes = 0 ;
    title3 'Figure 2 - Non-Febrile GI Infectious episode rate';

data freq_data;
    set freq_data;
    merge_flag = 1;

data person_year_data;
    merge freq_data
          mean_data;
    by merge_flag;
    infectious_rate = (count/person_years);

proc print data = person_year_data;

proc freq data = m81_data_part2;
    tables month_inf_reported /out = freq_data;
    where inf_epi_group = 2 and fever_yes = 1;
    title3 'Figure 2 - Febrile GI Infectious episode rate';

data freq_data;
    set freq_data;
    merge_flag = 1;

data person_year_data;
    merge freq_data
          mean_data;
    by merge_flag;

```

```

        infectious_rate = (count/person_years);

proc print data = person_year_data;

proc freq data = m81_data_part2;
    tables month_inf_reported /out = freq_data;
    where inf_epi_group = 3 and fever_yes = 0 ;
    title3 'Figure 2 - Non-Febrile Other Infectious episode rate';

data freq_data;
    set freq_data;
    merge_flag = 1;

data person_year_data;
    merge freq_data
          mean_data;
    by merge_flag;
    infectious_rate = (count/person_years);

proc print data = person_year_data;

proc freq data = m81_data_part2;
    tables month_inf_reported /out = freq_data;
    where inf_epi_group = 3 and fever_yes = 1;
    title3 'Figure 2 - Other Respiratory Infectious episode rate';

data freq_data;
    set freq_data;
    merge_flag = 1;

data person_year_data;
    merge freq_data
          mean_data;
    by merge_flag;
    infectious_rate = (count/person_years);

proc print data = person_year_data;

proc freq data = m81_data_part2;
    tables month_inf_reported /out = freq_data;
    where inf_epi_group = 4;
    title3 'Figure 2 - Unknown Febrile Infectious episode rate';

data freq_data;
    set freq_data;
    merge_flag = 1;

data person_year_data;
    merge freq_data
          mean_data;
    by merge_flag;

```



```

        infectious_rate = (count/person_years);

proc print data = person_year_data;

*** Figure 3 - Use calculated 'infectious_rate' variable to create graphs in Excel;

data mean_data;
    set mean_data;
    age_person_years = sum/16;

proc means data = m81_data_part3 n sum;
    var sum_inf_fever;
    class visit;
    output out = age_mean_data sum = age_sum;
    title3 'Figure 3 - Infectious Rate All Febrile Infectious Episodes';

data age_mean_data;
    set age_mean_data;
    merge_flag = 1;

data person_year_data;
    merge age_mean_data
          mean_data;
    by merge_flag;
    infectious_rate = (age_sum/age_person_years);
    if _type_ = 1;

proc print data = person_year_data;

proc means data = m81_data_part3 n sum;
    var sum_inf_no_fever;
    class visit;
    output out = age_mean_data sum = age_sum;
    title3 'Figure 3 - Infectious Rate All Non-Febrile Infectious Episodes';

data age_mean_data;
    set age_mean_data;
    merge_flag = 1;

data person_year_data;
    merge age_mean_data
          mean_data;
    by merge_flag;
    infectious_rate = (age_sum/age_person_years);
    if _type_ = 1;

proc print data = person_year_data;

proc means data = m81_data_part3 n sum;
    var sum_respir_all;
    class visit;

```

```

        output out = age_mean_data sum = age_sum;
        title3 'Figure 3 - Infectious Rate All Respiratory Infectious Episodes';

data age_mean_data;
    set age_mean_data;
    merge_flag = 1;

data person_year_data;
    merge age_mean_data
          mean_data;
    by merge_flag;
    infectious_rate = (age_sum/age_person_years);
    if _type_ = 1;

proc print data = person_year_data;

proc means data = m81_data_part3 n sum;
    var sum_gastro_all;
    class visit;
    output out = age_mean_data sum = age_sum;
    title3 'Figure 3 - Infectious Rate All GI Infectious Episodes';

data age_mean_data;
    set age_mean_data;
    merge_flag = 1;

data person_year_data;
    merge age_mean_data
          mean_data;
    by merge_flag;
    infectious_rate = (age_sum/age_person_years);
    if _type_ = 1;

proc print data = person_year_data;

proc means data = m81_data_part3 n sum;
    var sum_ICD_all;
    class visit;
    output out = age_mean_data sum = age_sum;
    title3 'Figure 3 - Infectious Rate All Other Infectious Episodes';

data age_mean_data;
    set age_mean_data;
    merge_flag = 1;

data person_year_data;
    merge age_mean_data
          mean_data;
    by merge_flag;
    infectious_rate = (age_sum/age_person_years);
    if _type_ = 1;

```

```

proc print data = person_year_data;

proc means data = m81_data_part3 n sum;
  var sum_fever_only_all;
  class visit;
  output out = age_mean_data sum = age_sum;
  title3 'Figure 3 - Infectious Rate All Unknown Febrile Infectious Episodes';

data age_mean_data;
  set age_mean_data;
  merge_flag = 1;

data person_year_data;
  merge age_mean_data
        mean_data;
  by merge_flag;
  infectious_rate = (age_sum/age_person_years);
  if _type_ = 1;

proc print data = person_year_data;

*** Using the code below, use the mean of the reference variable ("Reference Mean") and divide the mean, lower mean, and upper mean
*** for the other variables by the Reference Mean to obtain the RR and 95% CI for these variables;

proc genmod data = m81_data_part3;
  class cc (ref='1') fdr (ref='0') female (ref='1') hla_5grps (ref='2');
  model sum_inf_all = cc fdr female hla_5grps /dist = poisson ;
  lsmeans cc /ilink cl;
  run;
  title3 'Any Infection episode rate ratios - Site';

proc genmod data = m81_data_part3;
  class cc (ref='1') fdr (ref='0') female (ref='1') hla_5grps (ref='2');
  model sum_inf_all = cc fdr female hla_5grps /dist = poisson ;
  lsmeans female /ilink cl;
  run;
  title3 'Any Infection episode rate ratios - Gender';

proc genmod data = m81_data_part3;
  class cc (ref='1') fdr (ref='0') female (ref='1') hla_5grps (ref='2');
  model sum_inf_all = cc fdr female hla_5grps /dist = poisson ;
  lsmeans fdr /ilink cl;
  run;
  title3 'Any Infection episode rate ratios - First degree relative with T1D';

proc genmod data = m81_data_part3;
  class cc (ref='1') fdr (ref='0') female (ref='1') hla_5grps (ref='2');
  model sum_inf_all = cc fdr female hla_5grps /dist = poisson ;
  lsmeans hla_5grps /ilink cl;
  run;

```

```

title3 'Any Infection episode rate ratios - HLA-Dr-Dq genotype';

proc genmod data = m81_data_part3;
  class cc (ref='1') fdr (ref='0') female (ref='1') hla_5grps (ref='2');
  model sum_inf_fever = cc fdr female hla_5grps /dist = poisson ;
  lsmeans cc /ilink cl;
run;
title3 'Febrile infectious episode rate ratios - Site';

proc genmod data = m81_data_part3;
  class cc (ref='1') fdr (ref='0') female (ref='1') hla_5grps (ref='2');
  model sum_inf_fever = cc fdr female hla_5grps /dist = poisson ;
  lsmeans female /ilink cl;
run;
title3 'Febrile infectious episode rate ratios - Gender';

proc genmod data = m81_data_part3;
  class cc (ref='1') fdr (ref='0') female (ref='1') hla_5grps (ref='2');
  model sum_inf_fever = cc fdr female hla_5grps /dist = poisson ;
  lsmeans fdr /ilink cl;
run;
title3 'Febrile infectious episode rate ratios - First degree relative with T1D';

proc genmod data = m81_data_part3;
  class cc (ref='1') fdr (ref='0') female (ref='1') hla_5grps (ref='2');
  model sum_inf_fever = cc fdr female hla_5grps /dist = poisson ;
  lsmeans hla_5grps /ilink cl;
run;
title3 'Febrile infectious episode rate ratios - HLA-DR-DQ Genotype';

proc genmod data = m81_data_part3;
  class cc (ref='1') fdr (ref='0') female (ref='1') hla_5grps (ref='2');
  model sum_inf_no_fever = cc fdr female hla_5grps /dist = poisson ;
  lsmeans cc /ilink cl;
run;
title3 'Non-febrile infectious episode rate ratios - Site';

proc genmod data = m81_data_part3;
  class cc (ref='1') fdr (ref='0') female (ref='1') hla_5grps (ref='2');
  model sum_inf_no_fever = cc fdr female hla_5grps /dist = poisson ;
  lsmeans female /ilink cl;
run;
title3 'Non-febrile infectious episode rate ratios - Gender';

proc genmod data = m81_data_part3;
  class cc (ref='1') fdr (ref='0') female (ref='1') hla_5grps (ref='2');
  model sum_inf_no_fever = cc fdr female hla_5grps /dist = poisson ;
  lsmeans fdr /ilink cl;
run;
title3 'Non-febrile infectious episode rate ratios - First degree relative with T1D';

```

```
proc genmod data = m81_data_part3;
  class cc (ref='1') fdr (ref='0') female (ref='1') hla_5grps (ref='2');
  model sum_inf_no_fever = cc fdr female hla_5grps /dist = poisson ;
  lsmeans hla_5grps /ilink cl;
run;
title3 'Non-febrile infectious episode rate ratios - HLA-DR-DQ Genotype';
```