Dataset Integrity Check for the TrialNet-05 Rituximab Anti-CD20 Study

Prepared by

RTI International
3040 Cornwallis Road
Research Triangle Park, NC 27709-2194
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Revision History

Version	Author/Title	Date	Comments
1.0	SM Rogers/TN-05 DSIC	October 12, 2012	Original

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1 Introduction

The TN-05 study is a two-arm, randomized, double-blind, placebo-controlled clinical trial conducted as part of the TrialNet Type 1 Diabetes studies. This multi-center trial was conducted at 13 sites with subjects 8–45 years of age diagnosed with autoimmune type 1 diabetes for less than 3 months. Participants were randomized 2:1 to receive infusions of rituximab, an anti-CD20 monoclonal antibody, or placebo. As a partial check of the TN-05 data archived in the NIDDK data repository, a dataset integrity check (DSIC) was performed to verify that selected published results from the TN-05 study can be reproduced using the archived dataset. This DSIC consists of several analyses performed to duplicate selected results reported by Pescovitz et al in the *New England Journal of Medicine* in 2009 [1].

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 on a first (or second) exercise 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 objective of this study was to assess the safety, efficacy, and mode of action of rituximab, an anti-CD20 monoclonal antibody, for the treatment of individuals with new onset type 1 diabetes. Study participants received infusions of rituximab or placebo on days 1, 8, 15, and 22 of the study. The primary statistical hypothesis to be assessed was whether the mean C-peptide value for study subjects on rituximab differed significantly from the mean value for placebo subjects assessed at one year of follow-up. The study examined the effect of the proposed treatment on surrogate markers for immunologic effects, namely disease-specific outcomes and immunological outcomes.

The paper by Pescovitz et al (2009) provides the main study results for the efficacy trial.

3 Archived Datasets

The DCC submitted 27 datasets; the correspondence between study data sets and study data collection forms is provided in the TN-05 NIDDK Repository Roadmap.

Analysis datasets to correspond with published results by the TN-05 study group were not provided and reconstruction of the analysis dataset and derived variables were conducted by repository analysts. For this DSIC, we used the following TN-05 datasets: treatment_table; screening_form; baseline_med_hist; study_drug_admin; cbc_wdiff_results; research_labs; and diabetes_management. Our DSIC analyses were conducted in Stata v12 (Appendix 1). SAS datasets were converted to Stata using Stat/Transfer (Circle Systems Inc).

4 Statistical Methods

We present our DSIC results with the published results in:

- Table 1, Characteristics of the study groups, and
- Figure 2, Effects of rituximab on C-peptide level, glycated hemoglobin level, insulin dose required, CD19+ cell counts, and IgM level *(for this DSIC analysis we present results for three subfigures, glycated hemoglobin, insulin dose and IgM level).*

A total of 126 patients between 8 and 45 years of age who had type 1 diabetes were screened at 12 clinical sites for the presence of at least one detectable diabetes autoantibody: MIAA, GAD, ICA-512, or ICA. Enrollment occurred between May 2006 and August 2007; all patients completed year-one follow-up by August 2008. The initial patients enrolled were 12 years of age and older. Eligible patients were randomized in a 2:1 ratio of active treatment versus placebo, stratified by clinical center.

As noted in the publication, the safety cohort consisted of 87 randomized patients. The effectiveness analyses were based on the pre-specified intention to treat cohort of 81 patients that excluded 1 patient whose consent was withdrawn before the initial infusion and 5 patients whose infusions were suspended.

5 Results

Characteristics of the Study Groups.

Table 1 provides characteristics of the 87 patients who underwent randomization in the published manuscript and our DSIC analyses. Study datasets and variable names used in our DSIC tabulations also are provided [we use the format *dataset name.variable name*]. Our DSIC results match closely the published results for several demographic characteristics and physical measurements, however our DSIC tabulations were unable to replicate the published number of autoantibodies present (MIAA, GAD65, ICA, ICA512) based on the laboratory results (OUTCOME) in the file research_labs. Several other differences are indicated [Note that discrepancies between the published and DSIC calculations are highlighted in Table 1]. For the laboratory autoantibody results, our DSIC estimates were based on a smaller number of observations. Our analyses suggest also a higher percentage of rituximab patients with DR4-DQ8 alleles present (56% v 33% in the manuscript; we note that our DSIC tabulations are based on 49 observations with non-missing values in the Rituximab group and 23 observations in the placebo group). Our DSIC calculations do not exactly match published results for the mean number of days since diagnosis or for the mean number of days between diagnosis and infection (although our base Ns match the published Ns); this difference may be associated with the selection of a different visit date variable from the data files that were merged to tabulate this estimate. Finally we note that we were unable to identify the study variable in the repository datasets to calculate the CD19+ and CD20+ results.

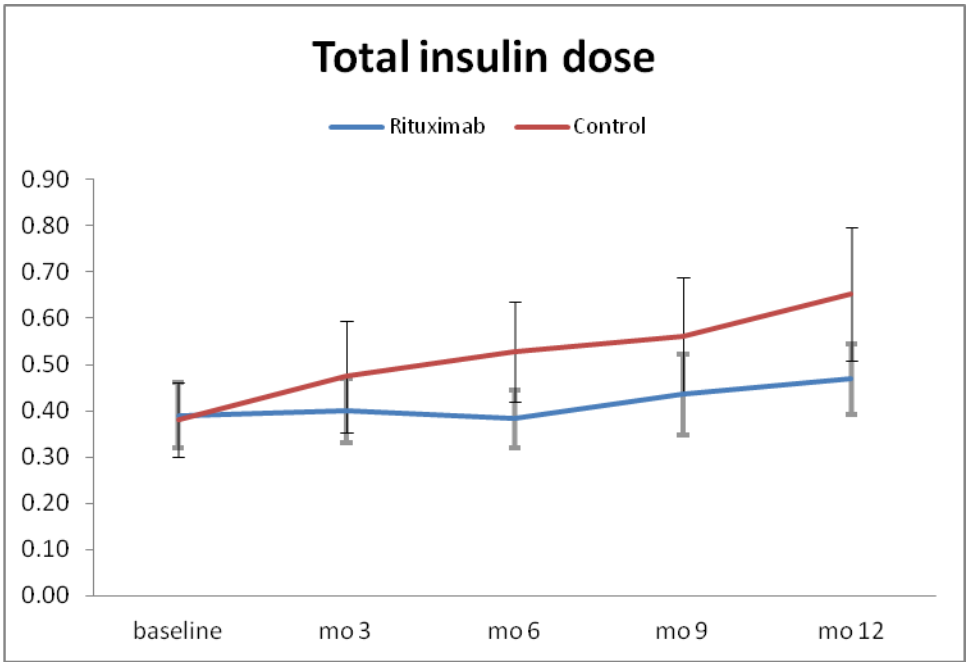
Table 1: Characteristics of the Study Groups.

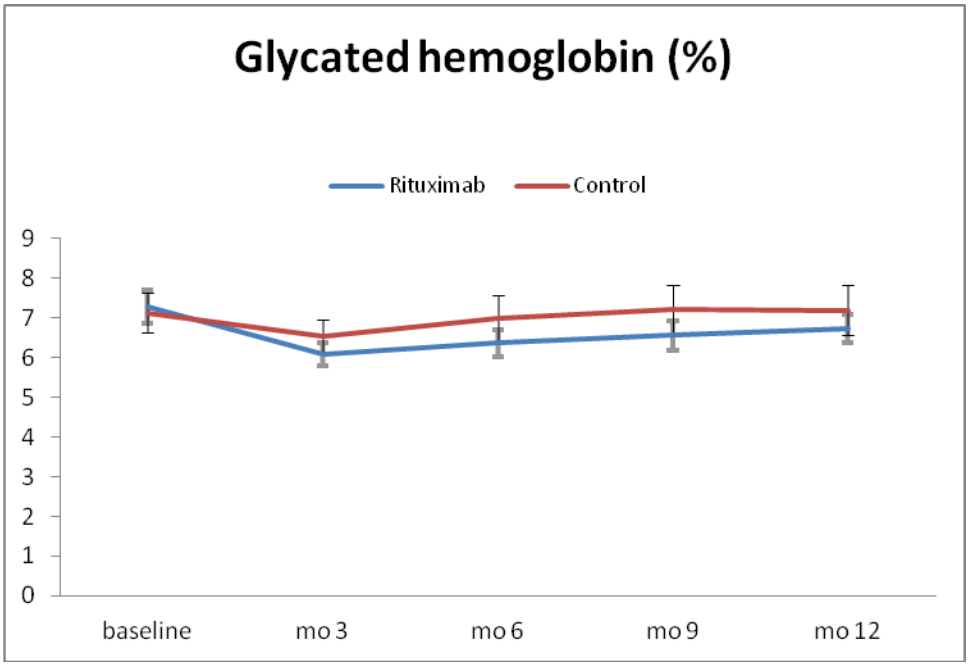
	Var.name	*from Pescovitz et al (2011)*		*DSIC analysis*	
	treatment_table.TreatmentName,Randomization_Date	**Rituximab**	**Placebo**	**Rituximab**	**Placebo**
		(N=57)	**(N=30)**	**(N=57)**	**(N=30)**
Age – yr	screening_form.Age				
Mean		19 ± 8.6	17.3 ± 7.8	19 ± 8.6	17.3 ± 7.8
Median		16	14	16	14
Range		8-40	9-38	8-40	9-38
Male sex -- no. of patients (%)	screening_form.sex	36 (63)	18 (60)	36 (63)	18 (60)
Race or ethnic group -- no. of patients (%) †	screening_form.Ethnicity, Race_[AmerInd,Asian, Black,NativeH,Other,White]				
White		55 (96)	29 (97)	54 (96)	29 (97)
Non-hispanic		54 (95)	27 (90)	54 (95)	27 (90)
No. of autoantibodies -- no. of patients (%)	research labs.TEST_NAME, Visit=Screening				
1	[TEST_NAME=MIAA]	10 (18)	3 (10)	not calculated	
2	[TEST_NAME=GAD65]	18 (32)	7 (23)	not calculated	
3	[TEST_NAME=ICA512]	17 (30)	9 (30)	not calculated	
4	[TEST_NAME=ICA]	12 (21)	11(37)	not calculated	
No. of days since diagnosis	baseline_med_hist.Date_at_T1DDiag,Date_at_visit	80±22	83 ± 19	83±22	87±14
No. of days from diagnosis to first infusion	study_drug_admin.Visit, Date_of_Visit,				
Median		81	91	88	91
Range		37-137	34-109	37-137	56-109
Weight (kg)	study_drug_admin.WeightInKgs	66±21.9	58 ± 16.8	66±21.9	58 ± 16.8
Body-mass index	study_drug_admin.WeightInKgs,HeightInCms	23.2±5.2	21.2 ± 4.3	23.2±5.2	21.2 ± 4.3
Total white cells -- per mm^3	cbc_wdiff_results.WBCresult	5500±1500	4900 ± 1200	5500±1500	4900 ± 1200
CD19+ B cells lymphocytes -- per mm^3	??	275.23±134.74	338.02±226.13	not calculated	
CD20+ B cells lymphocytes -- per mm^3	??	268.58±127.41	295.85±122.15	not calculated	
Mean AUC for C peptide -- pmol/ml	research_labs.TEST_NAME=PEP120	0.75±0.39	0.74 ± 0.37	not calculated	
Glycated hemoglobin at baseline -- %	research_labs.TEST_NAME=HbA1c, Visit=Screening	7.31±1.46	7.08 ± 1.28	7.28±1.5	7.13±1.31

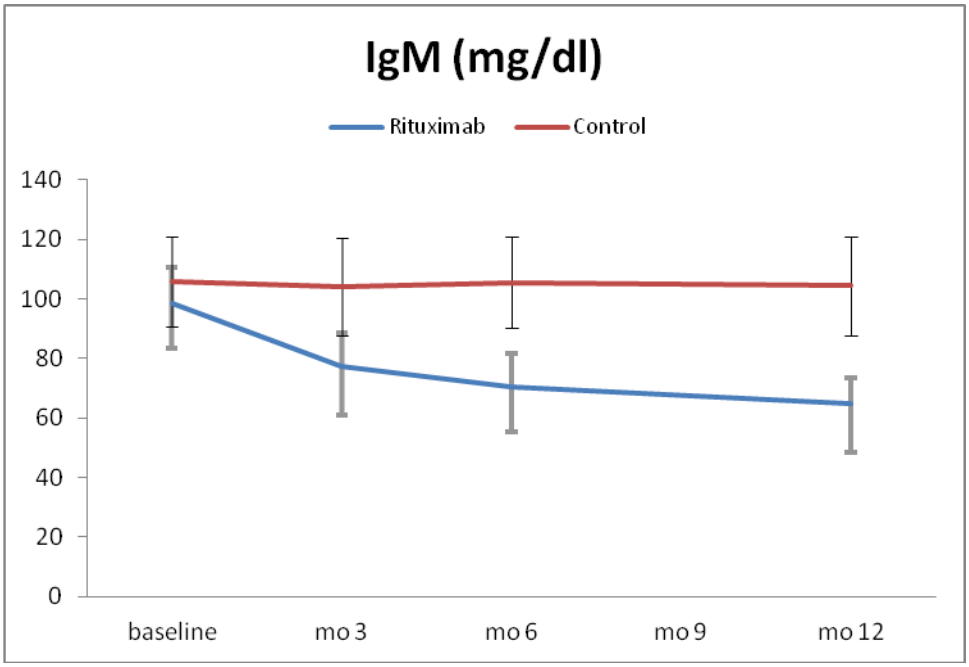
	Var.name	*from Pescovitz et al (2011)*		*DSIC analysis*	
	treatment_table.TreatmentName,Randomization_Date	**Rituximab**	**Placebo**	**Rituximab**	**Placebo**
		(N=57)	**(N=30)**	**(N=57)**	**(N=30)**
Total insulin dose (units/kg)	diabetes_management.AvgUnitsShortActingInsulin AverageUnitsOfItermediateInsul; weightInKg	0.37±0.24	0.38 ± 0.22	0.39±0.24 **	0.38±0.22 **
Diabetes-associated HLA alleles present					
--no. of patients (%)					
DR3-DQ2	research_labs.TEST_NAME=DR3	25 (44)	12 (40)	24 (42)‡	9 (30)‡
DR4-DQ8	research_labs.TEST_NAME=DR4	19 (33)	14 (47)	32 (56)‡	16 (53)‡
DR3-DQ2 and DR4-DQ8	research_labs.TEST_NAME=DR3, DR4	12 (21)	7 (23)	11 (22)‡	3 (13)‡
Received all 4 full infusions -- no. of patients (%)	study_drug_admin.FullDoseInfused,VisitNumber	46 (81)	28 (93)	48 (84)‡	28 (93)‡
* Plus-minus values are means±SD. The body-mass index is the weight in kilograms divided by the square of the height in meters. AUC denotes area under the curve.					
†Race was self-reported.					
DSIC Notes: Number of days since T1D diagnosis calculated from date of baseline visit from baseline_med_hist. Date of first infusion calculated from baseline visit date in study_drug_admin. ** Base N=50 for Rituximab and N=29 for placebo ‡ Tabulations for HLA alleles exclude 8 missing values for Rituximab and 7 missing values for placebo group.					

Rituximab Effectiveness. Effectiveness data are presented in Figure 1. The effectiveness analyses were based on a predefined intention-to-treat cohort of 81 patients. For this DSIC, we present levels of glycated hemoglobin (Fig 1B), total insulin dose (Fig 1C), and IgM (Fig 1E) over the 12-month follow-up period. Our DSIC results match trends presented in the published figures. Compared with the placebo group, the rituximab group had lower levels of HbA1C over the 12-month period, required lower insulin doses per kilogram of body weight, and had lower IgM levels. In addition to replicating the figures, we present our DSIC estimates used to tabulate the three subfigures. Our DSIC calculations match closely the estimates presented in Figure 2 (2B, 2C, and 2E) of the manuscript.

Figure 1. Effects of Rituximab on Glycated Hemoglobin Level, Insulin Dose Required, and IgM Level

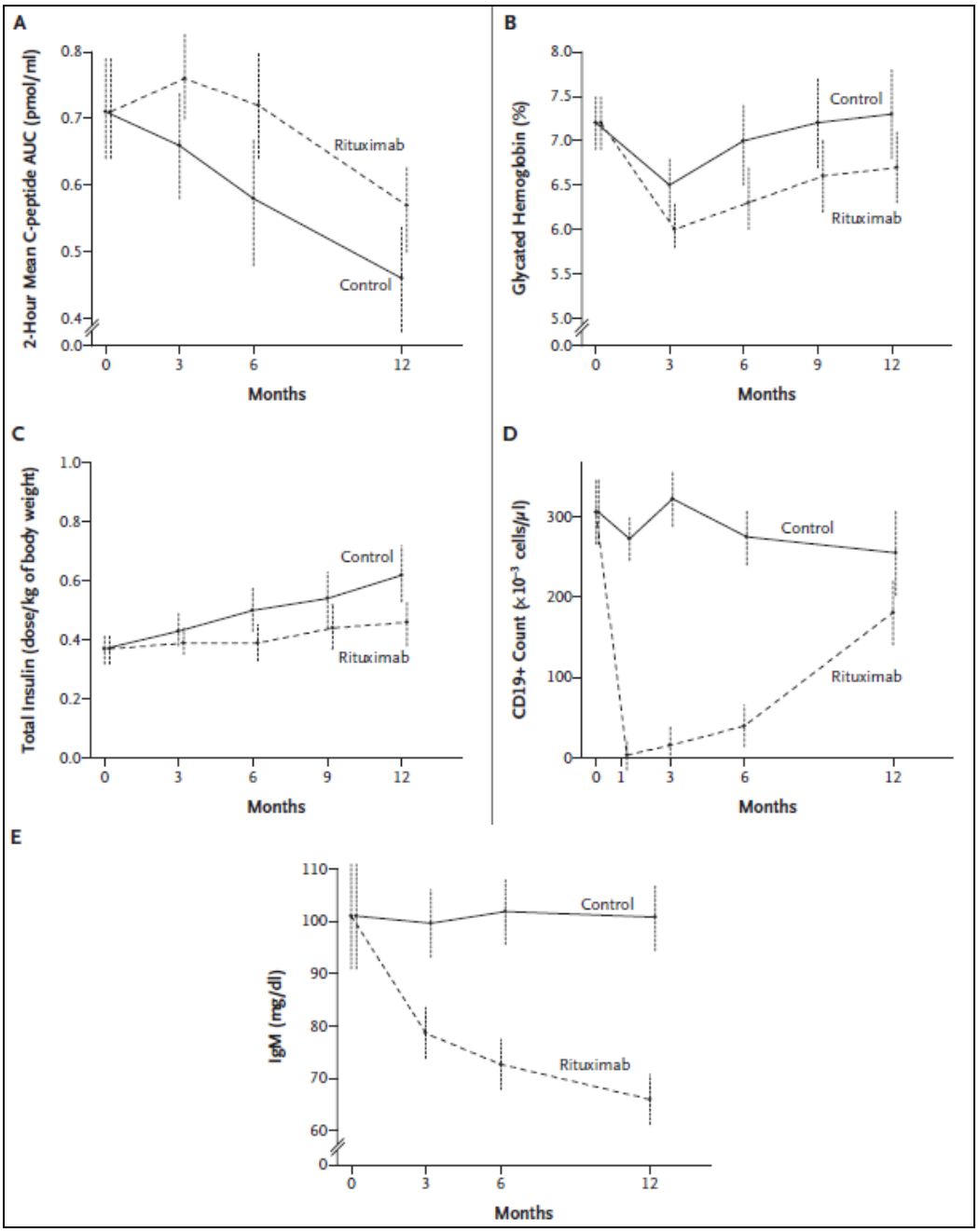






		Rituximab				Placebo		
Total Insulin	**N**	**Mean**	**95% Conf. Int.**		**N**	**Mean**	**95% Conf. Int.**	
Baseline	50	0.39	0.32	0.46	29	0.38	0.3	0.46
Month 3	49	0.40	0.33	0.47	28	0.47	0.35	0.59
Month 6	48	0.38	0.32	0.45	29	0.53	0.42	0.64
Month 9	47	0.44	0.35	0.52	26	0.56	0.44	0.69
Month 12	45	0.47	0.39	0.55	29	0.65	0.51	0.80
IgM								
Baseline	56	98.46	86.13	110.80	29	105.72	90.55	120.90
Month 3	53	77.37	66.18	88.57	30	104.13	87.61	120.66
Month 6	51	70.59	59.32	81.8	30	105.47	90.12	120.81
Month 9	0				0			
Month 12	56	64.79	56.02	73.56	28	104.39	87.91	120.87
HbA1C								
Baseline	53	7.28	6.87	7.69	28	7.12	6.62	7.63
Month 3	54	6.09	5.80	6.38	29	6.53	6.12	6.94
Month 6	52	6.36	6.03	6.69	30	6.99	6.39	7.58
Month 9	50	6.55	6.16	6.94	29	7.20	6.58	7.82
Month 12	52	6.74	6.39	7.09	29	7.19	6.55	7.83

Figure 2: Pescovitz et al. Effects of Rituximab on C-Peptide Level, Glycated Hemoglobin Level, Insulin Dose Required, CD19+ Cell Counts, and IgM Level.



Note: For each panel, 95% confidence limits are shown at each time point within each group.

6 Conclusions

Our DSIC analyses are similar to the results published by Pescovitz and colleagues (2009). We note that were unable to fully replicate laboratory results for several outcome measures in part because of our inability to identify a study variable in the repository data to estimate CD19+ and CD20+ B cell lymphocytes reported in Table 1 and Figure 2. Otherwise, the results of this DSIC suggest that the data provided to the NIDDK repository include the range of study variables and data collection instruments from the TN-05 study and show no obvious evidence of corruption in storage, transmission, or processing by repository staff.

7 References

[1] Pescovitz MD et al for the Type 1 Diabetes TrialNet Anti-CD20 Study Group. 2009. Rituximab, B-Lymphotcye depletion, and preservation of beta-cell function. *New England Journal of Medicine* 361:2143-52.

[2] Appendix

STATA v12 log of programming code for DSIC analysis of Pescovitz et al (2009) manuscript in *New England Journal of Medicine.*

Appendix 1.

```
use "C:\Documents and Settings\smr\My Documents\TrialNet\Rituximab Study (TN-05)\Data4
August2012\5\Stata\treatment_table.dta", clear

tab TreatmentName if Randomization_Date !=.
*n=115, 40 placebo 75 rituximab
keep TreatmentName MaskID Randomization_Date
keep if Randomization_Date !=.
save "C:\Documents and Settings\smr\My Documents\TrialNet\Rituximab Study (TN-05)\DSIC\rand.dta", replace

 use "C:\Documents and Settings\smr\My Documents\TrialNet\Rituximab Study (TN-05)\Data4
August2012\5\Stata\screening_form.dta", clear
 tab Visit sex
keep if Visit=="Screening"
tab1 Age sex Ethnicity Race_AmericanInd Race_Asian Race_Black Race_Other Race_White Race_NativeHaw
summ Age, detail
keep Age sex Ethnicity Race_AmericanInd Race_Asian Race_Black Race_Other Race_White Race_NativeHaw MaskID
sort MaskID
merge m:m MaskID using "C:\Documents and Settings\smr\My Documents\TrialNet\Rituximab Study (TN-05)\DSIC\rand.dta"
keep if _merge==3
save "C:\Documents and Settings\smr\My Documents\TrialNet\Rituximab Study (TN-05)\DSIC\randscr.dta", replace

use "C:\Documents and Settings\smr\My Documents\TrialNet\Rituximab Study (TN-05)\Data4
August2012\5\Stata\baseline_med_hist.dta", clear
  *n=115
gen dayst1d= Date_of_Visit-Date_At_T1DDiag
summ dayst1d
keep dayst1d Date_At_T1DDiag MaskID
sort MaskID
merge m:m MaskID using "C:\Documents and Settings\smr\My Documents\TrialNet\Rituximab Study (TN-
05)\DSIC\randscr.dta", gen(_merge2)
duplicates report
duplicates drop
save "C:\Documents and Settings\smr\My Documents\TrialNet\Rituximab Study (TN-05)\DSIC\demo.dta", replace
*n=87

 use "C:\Documents and Settings\smr\My Documents\TrialNet\Rituximab Study (TN-05)\Data4
August2012\5\Stata\study_drug_admin.dta", clear
tab WeightinKg if Visit=="Baseline", missing
gen weightkg=WeightinKg if Visit=="Baseline"
replace weightkg=WeightinLbs/2.2 if WeightinKg==. & Visit=="Baseline"
tab weightkg, missing
tab heightinCm if Visit=="Baseline", missing
gen heightcm=heightinCm if Visit=="Baseline"
replace heightcm=heightinInches*2.54 if heightinCm==. & Visit=="Baseline"
tab heightcm, missing
tab Date_of_Visit if Visit=="Baseline"
gen date1inf=Date_of_Visit if Visit=="Baseline"
tab date1inf
gen bmi=weightkg/(heightcm)*(heightcm) if Visit=="Baseline"
tab bmi, missing
tab weightkg Visit

tab GivenThereIVinfusionAtThisVisi Visit
*protocol at day 1,8,15 and 22
gen infusion=.
```

```
replace infusion =1 if GivenThereIVinfusionAtThisVisi=="Yes"
replace infusion =0 if GivenThereIVinfusionAtThisVisi=="No"
encode Visit, gen(visit)
tab infusion visit
keep weightkg heightcm date1inf bmi infusion visit MaskID
sort MaskID

reshape wide weightkg heightcm date1inf bmi infusion, i(MaskID) j(visit)
*duplicates drop in 143 drop in 305 Baseline visits duplicate
  *n=87
tab1 infusion*
egen totinf = rowtotal (infusion*)
tab totinf
keep MaskID weightkg4 heightcm4 date1inf4 bmi4 infusion1 infusion2 infusion3 infusion4 totinf
gen rand87=1
sort MaskID
save "C:\Documents and Settings\smr\My Documents\TrialNet\Rituximab Study (TN-05)\DSIC\drugadmin.dta", replace

merge 1:1 MaskID using "C:\Documents and Settings\smr\My Documents\TrialNet\Rituximab Study (TN-05)\DSIC\demo.dta",
gen(_merge3)

save "C:\Documents and Settings\smr\My Documents\TrialNet\Rituximab Study (TN-05)\DSIC\demodrug.dta", replace


use "C:\Documents and Settings\smr\My Documents\TrialNet\Rituximab Study (TN-05)\Data4
August2012\5\Stata\cbc_wdiff_results.dta", clear
tab Visit
tab WBCresults if Visit=="Baseline"
keep if Visit=="Baseline"
gen wbcbase=WBCresults
tab wbcbase
sort MaskID
keep MaskID wbcbase
merge m:m MaskID using "C:\Documents and Settings\smr\My Documents\TrialNet\Rituximab Study (TN-
05)\DSIC\demodrug.dta", gen(_merge4)

                        save "C:\Documents and Settings\smr\My Documents\TrialNet\Rituximab Study (TN-
05)\DSIC\demodrugcbc.dta", replace

                        ******************
use "C:\Documents and Settings\smr\My Documents\TrialNet\Rituximab Study (TN-05)\Data4
August2012\5\Stata\research_labs.dta", clear
keep if event_title=="Autoantibodies Specimen Collection"
sort TEST_NAME MaskID
by TEST_NAME:tab OUTCOME
keep if TEST_NAME=="MIAA" | TEST_NAME=="GAD65" | TEST_NAME=="ICA512" | TEST_NAME=="ICA"
keep if Date_of_Draw !=.
list MaskID TEST_NAME OUTCOME Date_of_Draw Visit
describe OUTCOME
label define posneg 1"Pos" 0"Neg"
encode OUTCOME, gen(outcome) label(posneg)
  /* keep first of each test result */
  by MaskID TEST_NAME (Date_of_Draw), sort: gen firstdate=Date_of_Draw[1]
format firstdate %tdd_m_y

merge m:m MaskID using "C:\Documents and Settings\smr\My Documents\TrialNet\Rituximab Study (TN-05)\DSIC\rand.dta",
gen(_merge9)
list MaskID TEST_NAME outcome Date_of_Draw firstdate TreatmentName
*keep if _merge9==3
by TreatmentName, sort:tab TEST_NAME OUTCOME
            /* Note: some patients with multiple results */
*label define autoanti 1"Pos" 0"Neg", replace
```

```
*encode OUTCOME, gen(aaoutcome) label(autoanti)
*list aaoutcome, nolabel
*by TreatmentName:tab TEST_NAME aaoutcome, nolabel
keep if firstdate==Date_of_Draw
keep MaskID TEST_NAME outcome
drop if TEST_NAME==""
drop in 42
reshape wide outcome, i(MaskID) j(TEST_NAME) string
describe

list outcome*, nolabel
egen totaa=rowtotal(outcomeGAD65 outcomeMIAA outcomeICA outcomeICA512)
tab totaa
sort MaskID
merge m:1 MaskID using "C:\Documents and Settings\smr\My Documents\TrialNet\Rituximab Study (TN-
05)\DSIC\demodrug.dta", gen(_merge5)
sort TreatmentName
by TreatmentName:summ outcome*
tab TreatmentName totaa
**********************


use "C:\Documents and Settings\smr\My Documents\TrialNet\Rituximab Study (TN-05)\Data4
August2012\5\Stata\research_labs.dta", clear
tab1 TEST_NAME Visit
tab RESULT if TEST_NAME=="PEP120"
tab Visit if TEST_NAME=="HbA1c"

keep if Visit=="Screening"
drop if TEST_NAME==""
keep if TEST_NAME=="DR3" | TEST_NAME=="DR4" | TEST_NAME=="MIAA" | TEST_NAME=="GAD65" |
TEST_NAME=="ICA512" | TEST_NAME=="ICA" | TEST_NAME=="HbA1c"
keep MaskID TEST_NAME RESULT
reshape wide RESULT, i(MaskID) j(TEST_NAME) string

gen hbres=RESULTHbA1c
destring hbres, replace
summ hbres
gen dr3res=RESULTDR3
gen dr4res=RESULTDR4
tab1 dr3res dr4res
gen dr3s=1 if dr3res=="PRESENT"
replace dr3s=0 if dr3res=="ABSENT"
gen dr4s=1 if dr4res=="PRESENT"
replace dr4s=0 if dr4res=="ABSENT"
tab1 dr3s dr4s

gen miaab=RESULTMIAA
gen gad65b=RESULTGAD65
gen ica512b=RESULTICA512
gen icab=RESULTICA
tab1 miaab gad65b ica512b icab
destring miaab gad65b ica512b icab, replace
sort MaskID
        save "C:\Documents and Settings\smr\My Documents\TrialNet\Rituximab Study (TN-05)\DSIC\labdata.dta", replace

merge m:m MaskID using "C:\Documents and Settings\smr\My Documents\TrialNet\Rituximab Study (TN-
05)\DSIC\demodrugcbc.dta", gen(_merge5)
keep if TreatmentName!=""
        save "C:\Documents and Settings\smr\My Documents\TrialNet\Rituximab Study (TN-05)\DSIC\demodrglab.dta",
replace
```

```
use "C:\Documents and Settings\smr\My Documents\TrialNet\Rituximab Study (TN-05)\Data4
August2012\5\Stata\diabetes_management.dta", clear

tab1 AvgUnitsShortActingInsulin AverageUnitsOfItermediateInsul if Visit=="Baseline"
summ AvgUnitsShortActingInsulin AverageUnitsOfItermediateInsul if Visit=="Baseline"
keep if Visit=="Baseline"
keep MaskID AvgUnitsShortActingInsulin AverageUnitsOfItermediateInsul
sort MaskID
duplicates report
duplicates drop
merge 1:1 MaskID using "C:\Documents and Settings\smr\My Documents\TrialNet\Rituximab Study (TN-
05)\DSIC\demodrglab.dta", gen(_merge6)
        save "C:\Documents and Settings\smr\My Documents\TrialNet\Rituximab Study (TN-05)\DSIC\final.dta", replace

        /**to convert insulin dose to units/kg
use "C:\Documents and Settings\smr\My Documents\TrialNet\Rituximab Study (TN-05)\Data4
August2012\5\Stata\diabetes_health_info.dta", clear
 tab  InsulinDoseLast24Hrs
  gen unitkg= InsulinDoseLast24Hrs/ WeightKg
  summ unitkg
sort Visit
by Visit:summ unitkg
                this file has no associated form and includes followup not baseline or screening visit**/


**For Table 1
tab TreatmentName
sort TreatmentName
by TreatmentName:summ Age, detail
tab sex TreatmentName, col
gen race=.
replace race=1 if Race_White==1
replace race=2 if Race_AmericanInd==1 | Race_Asian==1 | Race_Black==1 | Race_NativeHawaiian==1 |Race_Other==1
tab race
tab race TreatmentName, col
tab Ethnicity TreatmentName, col
by TreatmentName:summ dayst1d
gen t1ddate=Date_At_T1DDiag
gen daydxinf=date1inf4-t1ddate
tab daydxinf
gen bmi=weightkg4/((heightcm4)*(heightcm4))
by TreatmentName:summ daydxinf weightkg4 bmi wbcbase hbres, detail
gen insul=AvgUnitsShortActingInsulin + AverageUnitsOfItermediateInsul
gen units=insul/weightkg4
by TreatmentName: summ units
by TreatmentName:tab dr3s, missing
by TreatmentName: tab dr4s, missing
gen HLA=.
replace HLA=1 if dr3s==1 & dr4s==0
replace HLA=2 if dr4s==1 & dr3s==0
replace HLA=3 if dr3s==1 & dr4s==1
replace HLA=4 if dr3s==0 & dr4s==0
tab HLA TreatmentName, col
tab totinf TreatmentName, col

        save "C:\Documents and Settings\smr\My Documents\TrialNet\Rituximab Study (TN-05)\DSIC\final.dta", replace

**********TABLE 2. **********
use "C:\Documents and Settings\smr\My Documents\TrialNet\Rituximab Study (TN-05)\Data4
August2012\5\Stata\diabetes_management.dta", clear
tab Visit
```

```
keep if Visit=="Baseline" | Visit=="12 weeks" | Visit=="26 weeks" | Visit=="39 weeks" | Visit=="52 weeks"
encode Visit, gen(visit)
tab1 AvgUnitsShortActingInsulin AverageUnitsOfItermediateInsul
gen insul=AvgUnitsShortActingInsulin + AverageUnitsOfItermediateInsul
sort visit
by visit:summ insul
keep MaskID visit insul
reshape wide insul, i(MaskID) j(visit)
  *drop in 124 382
label var insul1 "ins 12 weeks"
label var insul2 "ins 26 weeks"
label var insul3 "ins 39 weeks"
label var insul4 "ins 52 weeks"
label var insul5 "ins baseline"
  save "C:\Documents and Settings\smr\My Documents\TrialNet\Rituximab Study (TN-05)\DSIC\insul", replace

use "C:\Documents and Settings\smr\My Documents\TrialNet\Rituximab Study (TN-05)\Data4
August2012\5\Stata\phys_exam.dta", clear
tab Visit
keep if Visit=="Baseline" | Visit=="12 weeks" | Visit=="26 weeks" | Visit=="39 weeks" | Visit=="52 weeks"
encode Visit, gen(visit)
            /* Note this file only includes followup visits--baseline data for insulin from table 1 tabs above */
keep MaskID visit Weightkg  Weightlbs
sort visit
replace Weightkg=Weightlbs/2.2 if Weightkg==.
duplicates list
duplicates drop
keep MaskID visit Weightkg
reshape wide Weightkg, i(MaskID) j(visit)
***Note: estimates may not match because of dropped duplicate obs
label var Weightkg1 "weight 12 weeks"
label var Weightkg2 "weight 26 weeks"
label var Weightkg3 "weight 39 weeks"
label var Weightkg4 "weight 52 weeks"
merge 1:1 MaskID using "C:\Documents and Settings\smr\My Documents\TrialNet\Rituximab Study (TN-05)\DSIC\insul.dta",
gen(_merge8)
gen unit12=insul1/Weightkg1
gen unit26=insul2/Weightkg2
gen unit39=insul3/Weightkg3
gen unit52=insul4/Weightkg4
merge 1:1 MaskID using "C:\Documents and Settings\smr\My Documents\TrialNet\Rituximab Study (TN-05)\DSIC\final.dta",
gen(_merge9)
            save "C:\Documents and Settings\smr\My Documents\TrialNet\Rituximab Study (TN-05)\DSIC\tbl2_insul.dta",
replace
ci insul*
sort TreatmentName
by TreatmentName: ci insul*
gen unit00=insul5/weightkg4
by TreatmentName: ci unit*

use "C:\Documents and Settings\smr\My Documents\TrialNet\Rituximab Study (TN-05)\Data4
August2012\5\Stata\research_labs.dta", clear
keep if TEST_NAME=="HbA1c" | TEST_NAME=="PEP120" | TEST_NAME=="GLOIgM"
keep if Visit=="Screening" | Visit=="12 weeks" | Visit=="26 weeks" | Visit=="39 weeks" | Visit=="52 weeks"
encode Visit, gen(visit)
sort visit
gen result=real(RESULT)
*encode RESULT, gen(result)
keep MaskID TEST_NAME visit result
reshape wide result, i(MaskID TEST_NAME) j(visit)
label var result1 "result 12 wk"
label var result2 "result 26 wk"
```

```
label var result3 "result 39 wk"
label var result4 "result 52 wk"
label var result5 "result screening"

reshape wide result1 result2 result3 result4 result5, i(MaskID) j(TEST_NAME) string
merge 1:1 MaskID using "C:\Documents and Settings\smr\My Documents\TrialNet\Rituximab Study (TN-05)\DSIC\final.dta",
gen(_merge10)
sort TreatmentName
by TreatmentName:ci result*
        save "C:\Documents and Settings\smr\My Documents\TrialNet\Rituximab Study (TN-05)\DSIC\table2_other.dta",
replace
```