Dataset Integrity Check for the Chronic Renal Insufficiency Cohort (CRIC) Clinical Trial Data Files

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December 19, 2013

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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

Chronic kidney disease (CKD) is a public health epidemic that increases risk of death due to cardiovascular disease. Novel biomarkers may improve our ability to predict which patients with chronic kidney disease (CKD) are at higher risk for progressive loss of renal function. We assessed the performance of urine neutrophil gelatinase–associated lipocalin (NGAL) for outcome prediction in a diverse cohort of 3386 patients with CKD in the Chronic Renal Insufficiency Cohort study (CRIC). [1]

There is a great interest currently in defining novel biomarkers that will improve our ability to predict which patients with chronic kidney disease (CKD) are at higher risk for progressive loss of renal function, adding to currently available risk factors such as amount of total proteinuria and glomerular filtration rate (GFR). Better risk stratification may potentially improve clinical outcomes by facilitating the application or intensification of evidence-based therapies among higher-risk patients. [1]

One such promising novel biomarker is urine neutrophil gelatinase–associated lipocalin (NGAL). A recent comprehensive review identified urine NGAL as the most promising novel biomarker among those being evaluated as predictors of CKD progression. NGAL was originally identified in animal models by microarray analysis to be one of the earliest induced genes and proteins in the kidney after ischemic or nephrotoxic injury. It is a ubiquitous lipocalin iron-carrying protein, highly expressed in the tubular

epithelium, and released from tubular epithelial cells following damage. Although initially studied in the context of acute kidney injury, urine NGAL levels are also abnormally elevated (albeit at a much lower level) in a large number of individuals with CKD. [1]

A number of cross-sectional studies have shown that urine NGAL levels correlate with the level of GFR or severity of underlying renal parenchyma injury.5–10 Several small studies in selected populations have provided conflicting reports about whether urine NGAL is an independent risk factor of more rapid loss of renal function after controlling for established CKD progression risk factors (such as proteinuria and blood pressure level). [1]

In Chronic Renal Insufficiency Cohort study (CRIC), the baseline mean estimated glomerular filtration rate (eGFR) was 42.4ml/min per 1.73 square meter, the median 24-h urine protein was 0.2 g/day, and the median urine NGAL concentration was 17.2 ng/ml. Over an average follow-up of 3.2 years, there were 689 cases in which the eGFR was decreased by half or incident end-stage renal disease developed. Even after accounting for eGFR, proteinuria, and other known CKD progression risk factors, urine NGAL remained a significant independent risk factor (Cox model hazard ratio 1.70 highest to lowest quartile). The association between baseline urine NGAL levels and risk of CKD progression was strongest in the first 2 years of biomarker measurement. Within this time frame, adding urine NGAL to a model that included eGFR, proteinuria, and other CKD progression risk factors led to net reclassification improvement of 24.7%, but the C-statistic remained nearly identical. Thus, while urine NGAL was an independent risk factor of progression among patients with established CKD of diverse etiology, it did not substantially improve prediction of outcome events. [1]

3 Archived Datasets

All SAS data files, as provided by the Data Coordinating Center (DCC), are located in the CRIC "CRIC_Study_Data" folder in the data package. For this replication, variables were taken from five SAS derived data files, personlevel, , sa_allc, and sa_cvd, visitlevel_bl, visitlevel_long, containing both variables copied directly from the raw data files as well as calculated and categorical variables based on variables from the raw data files.

4 Statistical Methods

Analyses were performed to duplicate results for the data published by Liu et al [1] in Kidney International in January 2013.

To verify the integrity of the five SAS derived datasets, descriptive statistics of baseline characteristics and hazard ratio were computed, by overall of urine NGAL concentration (Table).

5 Results

Table 1 in the publication [1], Baseline patient characteristics: overall and by quintiles of urine NGAL concentration. Our Table A lists the variables we used in our replication and Table B compares the results calculated from the archived data file to the results published in Table 1. The results of the replication are similar to published results, within rounding error.

Table A: Variables Used to Replicate Table 1.

Measure	***Dataset.variable***
NGAL (ng/ml)	visitlevel_bl.NGAL
Sex	personlevel.SEX
Race	personlevel.RACE_ETHNICITY_CAT2
Diabetes	visitlevel_bl.Diabetes
Cardio-Vascular Disease	visitlevel_bl.ANYCVD
Ace inhibitor or ARB	visitlevel_bl.ACEARB
Age	visitlevel_bl.AGE
Urine Protein	visitlevel_bl.UPROTEIN24H
Estimated Glomerular Filtration Rate	visitlevel_long.EGFR_ROCHE
BMI	visitlevel_bl.BMI
Systolic	visitlevel_bl.SYSTOLIC
Diastolic	visitlevel_bl.DIASTOLIC

Table B: Table 1. Baseline patient characteristics: overall and by quintiles of urine NGAL concentration.

	<=6.9 [Manuscript]	<=6.9 [DSIC]	>6.9 to <=12.9 [Manuscript]	>6.9 to <=12.9 [DSIC]	>12.9 to <=22.6 [Manuscript]	>12.9 to <=22.6 [DSIC]
characteristic	681	680	678	678	673	673
Age,Mean (s.d.)	58.7 (10.3)	58.7 (10.3)	59.4 (10.0)	59.4 (10.0)	59.5 (10.9)	59.5 (10.9)
sex Female	103 (15.1%)	103 (15.1%)	258 (38.1%)	258 (38.1%)	381 (56.6%)	381 (56.6%)
race nonhispanic white	396 (58.1%)	396 (58.2%)	331 (48.8%)	331 (48.8%)	263 (39.1%)	263 (39.1%)
race nonhispanic black	206 (30.2%)	205 (30.1%)	277 (40.9%)	277 (40.9%)	314 (46.7%)	314 (46.7%)
race hispanic	40 (5.9%)	40 (5.9%)	43 (6.3%)	43 (6.3%)	76 (11.3%)	76 (11.3%)
Diabetes	303 (44.5%)	303 (44.6%)	270 (39.8%)	270 (39.8%)	304 (45.2%)	304 (45.2%)
24-h proteinuria Mean (s.d.)	0.3 (0.4)	0.3 (0.4)	0.5 (0.8)	0.5 (0.8)	0.7 (1.1)	0.7 (1.1)
24-h proteinuria Median (IQR)	0.1 (0.1,0.3)	0.1 (0.1,0.3)	0.1 (0.1,0.5)	0.1 (0.1,0.5)	0.2 (0.1,0.7)	0.2 (0.1,0.7)
Estimated GFR Mean (s.d.)	47.9 (12.0)	47.9 (12.0)	45.9 (12.4)	45.9 (12.4)	42.3 (12.7)	42.3 (12.7)
Estimated GFR Median (IQR)	48.0 (39.5,56.1)	48.0 (39.4,56.1)	44.7 (37.1,54.1)	44.7 (37.1,54.1)	41.2 (33.1,50.8)	41.2 (33.1,50.8)
Systolic BP Mean (s.d.)	123 (18)	123.0 (18.0)	126 (20)	126.0 (20.0)	127 (22)	127.0 (22.0)
Diastolic BP Mean (s.d.)	71 (12)	71.0 (12.0)	71 (12)	71.0 (12.0)	71 (13)	71.0 (13.0)
Body mass index Mean (s.d.)	31.2 (6.7)	31.2 (6.7)	31.6 (6.9)	31.6 (6.9)	32.3 (7.8)	32.3 (7.8)
History of cardiovascular disease	233 (34.2%)	232 (34.1%)	201 (29.6%)	201 (29.6%)	228 (33.9%)	228 (33.9%)
Use of ACE inhibitor or ARB	499 (73.7%)	498 (73.7%)	468 (69.5%)	468 (69.5%)	451 (67.3%)	451 (67.3%)
	>22.6 to <=49.5 [Manuscript]	>22.6 to <=49.5 [DSIC]	>49.5 [Manuscript]	>49.5 [DSIC]	ALL [Manuscript]	ALL [DSIC]
characteristic	677	677	677	677	3386	3385
Age,Mean (s.d.)	57.5 (11.3)	57.5 (11.3)	56.1 (11.9)	56.1 (11.9)	58.2 (11.0)	58.3 (11.0)
sex Female	444 (65.6%)	444 (65.6%)	406 (60.0%)	406 (60.0%)	1592 (47.0%)	1592 (47.0%)
race nonhispanic white	240 (35.5%)	240 (35.5%)	180 (26.6%)	180 (26.6%)	1410 (41.6%)	1410 (41.7%)
race nonhispanic black	332 (49.0%)	332 (49.0%)	311 (45.9%)	311 (45.9%)	1440 (42.5%)	1439 (42.5%)
race hispanic	83 (12.3%)	83 (12.3%)	162 (23.9%)	162 (23.9%)	404 (11.9%)	404 (11.9%)
Diabetes	357 (52.7%)	357 (52.7%)	400 (59.1%)	400 (59.1%)	1634 (48.3%)	1634 (48.3%)
24-h proteinuria Mean (s.d.)	1.2 (1.7)	1.2 (1.7)	3.1 (4.3)	3.1 (4.3)	1.1 (2.4)	1.1 (2.4)
24-h proteinuria Median (IQR)	0.3 (0.1,1.7)	0.3 (0.1,1.7)	1.1 (0.2,4.4)	1.1 (0.2,4.4)	0.2 (0.1,1.0)	0.2 (0.1,1.0)
Estimated GFR Mean (s.d.)	40.2 (13.6)	40.2 (13.6)	35.6 (13.5)	35.6 (13.5)	42.4 (13.6)	42.4 (13.6)
Estimated GFR Median (IQR)	38.0 (29.2,49.9)	38.0 (29.2,49.9)	33.8 (25.1,43.6)	33.8 (25.1,43.6)	41.6 (32.1,51.5)	41.6 (32.1,51.5)
Systolic BP Mean (s.d.)	131 (23)	131.0 (23.0)	137 (25)	137.0 (25.0)	129 (22)	129.0 (22.0)
Diastolic BP Mean (s.d.)	72(13)	72.0 (13.0)	73 (14)	73.0 (14.0)	72(13)	72.0 (13.0)
Body mass index Mean (s.d.)	33.5 (8.8)	33.5 (8.8)	32.5 (9.0)	32.5 (9.0)	32.2 (7.9)	32.2 (7.9)
History of cardiovascular disease	212 (31.3%)	212 (31.3%)	242 (35.7%)	242 (35.7%)	1116 (33.0%)	1115 (32.9%)
Use of ACE inhibitor or ARB	437 (64.9%)	437 (64.9%)	429 (64.0%)	429 (64.0%)	2284 (67.9%)	2283 (67.9%)

6 Conclusion

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

7 References

1. Kathleen D. Liu, Wei Yang, Amanda H. Anderson, Harold I. Feldman, Sevag Demirjian, Takayuki Hamano, Jiang He, James Lash, Eva Lustigova, Sylvia E. Rosas, Michael S. Simonson, Kaixiang Tao and Chi-yuan Hsu, on behalf of the Chronic Renal Insufficiency Cohort (CRIC) study investigators. Urine neutrophil gelatinase–associated lipocalin levels do not improve risk prediction of progressive chronic kidney disease. Kidney Int. 2013 January; 83, 909–914. Epub 2013 January 23.

Attachment A: SAS code

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

options nofmterr ps=60;

libname sas_data
"/prj/niddk/ims_analysis/CRIC/private_orig_data/CRIC_to_IMS_Nov2013/FTP_to_IMS_Nov2013/CRIC_Study
_Data/Derived_Data/";

*** Data from the Primary outcome paper that was converted to .csv format so that the DSIC data
could be easily compared;
FILENAME table1  '/prj/niddk/ims_analysis/CRIC/private_created_data/cric_table1_data.csv';
FILENAME table2  '/prj/niddk/ims_analysis/CRIC/private_created_data/cric_table2_data.csv';

*** Output CSV files that will be converted to .xls before being added to the DSIC document;
FILENAME out_t1_b  '/prj/niddk/ims_analysis/CRIC/private_created_data/cric_table1_dsic3.csv';

*** Reading in the analysis datasets used for the DSIC;
data personlevel      ; set sas_data.personlevel       ;
data sa_allc                          ; set sas_data.sa_allc;          ;
data sa_cvd           ; set sas_data.sa_cvd            ;
data visitlevel_bl    ; set sas_data.visitlevel_bl     ;
data visitlevel_long  ; set sas_data.visitlevel_long   ;

data all prob;
  merge visitlevel_bl(in = in1) personlevel (in = in2);
  by pid;
  if in1 and in2 then output all;
  else output prob;

proc sort data = all;
  by pid vnum;

proc sort data = VISITLEVEL_LONG(keep=pid vnum EGFR_ROCHE) ;
  by pid vnum;

data all prob;
  merge all(in = in1) VISITLEVEL_LONG (in = in2);
  by pid vnum;
  if in1 and in2 then output all;
  else if in1 and not in2 then output prob;

proc sort data = sa_allc ;
  by pid ;

data all prob;
  merge all(in = in1) sa_allc (in = in2);
  by pid ;
  if in1 and in2 then output all;
  else if in1 and not in2 then output prob;

*** Modifying, so that the NGAL_cat variable is in the same format as the manuscipt;
data all miss_NGAL nonspec_NGAL;
  set all;
  if NGAL <= 6.9 then NGAL_cat = 1;
  else if 6.9<NGAL<=12.9 then NGAL_cat = 2;
  else if 12.9<NGAL<=22.6 then NGAL_cat = 3;
  else if 22.6 < NGAL <=49.5 then NGAL_cat = 4;
  else if NGAL > 49.5 then NGAL_cat = 5;
  if SA_ALLC_ESRD = 1 then case = 1;
  else case = 0;

  if NGAL=. then output miss_NGAL;
  else if NGAL=5 then output nonspec_NGAL;

  else output all;
```

```
proc freq data = all;
  tables SA_ALLC_MDRD_RENAL1   NGAL_cat * (case SA_ALLC_DEATH SA_ALLC_CRIC_RENAL1 SA_ALLC_ESRD)
  SA_ALLC_ESRD * SA_ALLC_DEATH * NGAL_cat
  SA_ALLC_MDRD_RENAL1 * SA_ALLC_CRIC_RENAL1 * NGAL_cat
  /list missing;



*******************************************************************************;
*************** Check Table 1 ************************************************;
*******************************************************************************;

%macro baseline_freq(var_name);

       *** Creating a frequency table in the format of Table 1 in the primary outcome paper;
  proc freq data = ALL;
       table (&var_name.)*NGAL_cat;
       title2 "Frequency table of the &var_name. variable in the analysis dataset";

       *** Outputting the frequency data to work.&var_name._cross using the ODS output;
  ods output CrossTabFreqs = work.&var_name._cross;

  data &var_name._cross(keep = table NGAL_cat &var_name. first_stat second_stat);
    set &var_name._cross;
    if  &var_name. NE .;
        first_stat = frequency;
               second_stat = round(colpercent,0.1);
    if NGAL_cat = . then second_stat = round(Percent,0.1);
    if NGAL_cat = . then NGAL_cat = 6;

  proc transpose data=&var_name._cross out=&var_name._trans prefix=NGAL_cat;
     by &var_name.;


  data &var_name._trans ;
    set &var_name._trans;
    if _NAME_ = 'NGAL_cat' then delete;

  data &var_name._trans_count (rename = (NGAL_cat1 = NGAL_stat1 NGAL_cat2 = NGAL_stat4 NGAL_cat3
=NGAL_stat7 NGAL_cat4=NGAL_stat10 NGAL_cat5=NGAL_stat13 NGAL_cat6=NGAL_stat16))
       &var_name._trans_freq  (rename = (NGAL_cat1 = NGAL_stat2 NGAL_cat2 = NGAL_stat5 NGAL_cat3
=NGAL_stat8 NGAL_cat4=NGAL_stat11 NGAL_cat5=NGAL_stat14 NGAL_cat6=NGAL_stat17))
       ;
    set  &var_name._trans;
    if  _NAME_ = 'first_stat' then output &var_name._trans_count;
    else if _NAME_ = 'second_stat' then output &var_name._trans_freq;

  data &var_name._trans_merge(drop = _NAME_ );
    merge &var_name._trans_count (in = in1) &var_name._trans_freq (in = in2);
    by  &var_name.;
    if in1 and in2 then do;
      length table_name $ 30.;
      table_name = "&var_name.";
      group = &var_name.;
      output &var_name._trans_merge;
    end;
    else abort;

%mend;

%macro baseline_median(var_name);


       *** Creating a means table in the format of Table 1 in the primary outcome paper that
contain the median 25th percentile and 75th percentile;
  proc means data = all mean Std MEDIAN P25 P75 prt ;
    var &var_name.;
    by NGAL_cat;

       *** Outputting the statisitics to the work.&var_name._summary dataset using the ODS
output;
```

```
  ods output Summary = work.&var_name._summary;

  run;

  data &var_name._mean (keep =table_name NGAL_cat mean_stat sd_stat ) &var_name._median (keep
=table_name NGAL_cat median_stat p25_stat p75_stat );
    set &var_name._summary ;
    length table_name $ 30.;
    table_name = "&var_name.";
    Median_stat  = ROUND(&var_name._Median, 0.1);
    p25_stat = ROUND(&var_name._P25, 0.1);
    p75_stat  = ROUND(&var_name._P75, 0.1);
    mean_stat = ROUND(&var_name._mean, 0.1);
    sd_stat = ROUND(&var_name._StdDev, 0.1);

%mend;

%macro baseline_median_all(var_name);

       *** Creating a means table in the format of Table 1 in the primary outcome paper that
contain the median 25th percentile and 75th percentile;
  proc means data = all mean Std MEDIAN P25 P75 prt ;
    var &var_name.;

       *** Outputting the statisitics to the work.&var_name._summary dataset using the ODS
output;
  ods output Summary = work.&var_name._allsummary;

  run;

  data &var_name._allmean (keep =table_name NGAL_cat mean_stat sd_stat ) &var_name._allmedian
(keep =table_name NGAL_cat median_stat p25_stat p75_stat );
    set &var_name._allsummary ;
    length table_name $ 30.;
    table_name = "&var_name.";
    Median_stat  = ROUND(&var_name._Median, 0.1);
    p25_stat = ROUND(&var_name._P25, 0.1);
    p75_stat  = ROUND(&var_name._P75, 0.1);
    mean_stat = ROUND(&var_name._mean, 0.1);
    sd_stat = ROUND(&var_name._StdDev, 0.1);
    NGAL_cat= 6;
%mend;

*** Running the baseline_freq on the 6 categorical variables in the Table 1 manuscript file;
%baseline_freq(NGAL_cat   );
%baseline_freq(SEX   );
%baseline_freq(RACE_ETHNICITY_CAT2   );
%baseline_freq(Diabetes   );
%baseline_freq(ANYCVD   );
%baseline_freq(ACEARB   );

data NGAL_cat_trans_merge(keep = table_name NGAL_cat NGAL_stat16);
  set NGAL_cat_trans_merge;

proc transpose data=NGAL_cat_trans_merge out=NGAL_cat_trans  ;
   by table_name;
data NGAL_cat_trans(drop = _name_ rename = (COL1=NGAL_stat1 COL2=NGAL_stat4    COL3=NGAL_stat7
COL4=NGAL_stat10    COL5=NGAL_stat13));
  set NGAL_cat_trans;
  if _name_ = 'NGAL_stat16';
  NGAL_stat16 = COL1 + COL2 + COL3 + COL4 + COL5;

*** Creating a master Table 1 dataset using the baseline_freq and baseline_median datasets
created in the macros above;
*** This dataset is in the same order as the Table 1 SAS dataset taken from the Primary outcome
paper;
*** Note that some variables have two categories where the paper only described one of the two
categories;
*** (Ex. The Sex variable has both 1 (Male) and 2 (Female), however only the Female frequesncy
was included in the manuscript);
```

```
*** Setting the all freq datasets together;
data compare_freq (drop = sex RACE_ETHNICITY_CAT2 Diabetes ANYCVD ACEARB);
  set NGAL_cat_trans
      SEX_trans_merge                    (where = (group = 2))
      RACE_ETHNICITY_CAT2_trans_merge    (where = (group in (1,2,3)) )
      Diabetes_trans_merge               (where = (group = 1))
      ANYCVD_trans_merge                 (where = (group = 1))
      ACEARB_trans_merge                 (where = (group = 1)  )
;
  length category $12;
  category = 'count';

proc print data = compare_freq;
  title2 'compare_freq';

proc sort data = all;
  by NGAL_cat;


*** Running the baseline_media by category on the 6 continuous variables in the Table 1
manuscript file;
%baseline_median(age);
%baseline_median(UPROTEIN24H);
%baseline_median(EGFR_ROCHE);
%baseline_median(SYSTOLIC);
%baseline_median(DIASTOLIC);
%baseline_median(BMI);

*** Running the baseline_media on the 6 continuous variables in the Table 1 manuscript file;

%baseline_median_all(age);
%baseline_median_all(UPROTEIN24H);
%baseline_median_all(EGFR_ROCHE);
%baseline_median_all(SYSTOLIC);
%baseline_median_all(DIASTOLIC);
%baseline_median_all(BMI);


*** Setting the all mean datasets together;
data compare_mean_dataset(keep =  table_name NGAL_cat mean_stat sd_stat);
  set age_mean
      UPROTEIN24H_mean
      EGFR_ROCHE_mean
      SYSTOLIC_mean
      DIASTOLIC_mean
      BMI_mean
      age_allmean
      UPROTEIN24H_allmean
      EGFR_ROCHE_allmean
      SYSTOLIC_allmean
      DIASTOLIC_allmean
      BMI_allmean
      ;

proc sort data = compare_mean_dataset;
  by table_name ngal_cat;

proc transpose data=compare_mean_dataset out=compare_mean_dataset_trans prefix=NGAL_cat;
   by table_name;


data compare_median_dataset(keep =  table_name NGAL_cat median_stat p25_stat p75_stat);
  set
      UPROTEIN24H_median
      EGFR_ROCHE_median
      UPROTEIN24H_allmedian
      EGFR_ROCHE_allmedian
;
```

```
data compare_mean (drop = _name_ rename = (NGAL_cat1 = NGAL_stat1 NGAL_cat2 = NGAL_stat4
NGAL_cat3 =NGAL_stat7 NGAL_cat4=NGAL_stat10 NGAL_cat5=NGAL_stat13 NGAL_cat6=NGAL_stat16))
     compare_sd   (drop = _name_ rename = (NGAL_cat1 = NGAL_stat2 NGAL_cat2 = NGAL_stat5
NGAL_cat3 =NGAL_stat8 NGAL_cat4=NGAL_stat11 NGAL_cat5=NGAL_stat14 NGAL_cat6=NGAL_stat17))
     ;
  set compare_mean_dataset_trans;
  if _NAME_ = 'mean_stat' then output compare_mean;
  else if _NAME_ = 'sd_stat' then output compare_sd;

proc sort data = compare_median_dataset;
  by table_name ngal_cat;

proc transpose data=compare_median_dataset out=compare_median_dataset_trans prefix=NGAL_cat;
   by table_name;

data compare_median (drop = _name_ rename = (NGAL_cat1 = NGAL_stat1 NGAL_cat2 = NGAL_stat4
NGAL_cat3 =NGAL_stat7 NGAL_cat4=NGAL_stat10 NGAL_cat5=NGAL_stat13 NGAL_cat6=NGAL_stat16))
     compare_p25    (drop = _name_ rename = (NGAL_cat1 = NGAL_stat2 NGAL_cat2 = NGAL_stat5
NGAL_cat3 =NGAL_stat8 NGAL_cat4=NGAL_stat11 NGAL_cat5=NGAL_stat14 NGAL_cat6=NGAL_stat17))
     compare_p75    (drop = _name_ rename = (NGAL_cat1 = NGAL_stat3 NGAL_cat2 = NGAL_stat6
NGAL_cat3 =NGAL_stat9 NGAL_cat4=NGAL_stat12 NGAL_cat5=NGAL_stat15 NGAL_cat6=NGAL_stat18))
     ;
  set compare_median_dataset_trans;
  if _NAME_ = 'Median_stat' then output compare_median;
  else if _NAME_ = 'p25_stat' then output compare_p25;
  else if _NAME_ = 'p75_stat' then output compare_p75;

data compare_allmean;
  merge  compare_mean
         compare_sd
           ;
  by table_name;
  length category $12;
  category = 'mean';

*** Merging the three meidan datasets together;
data compare_allmedian;
  merge
         compare_median
         compare_p25
         compare_p75
           ;
  by table_name;
  length category $12;
  category = 'median';

*** Setting the Freq, Mean, and meidan datasets together;
data compare_dataset;
  set compare_freq  compare_allmean  compare_allmedian;
  table_name = upcase(table_name);
  length char_compare_stat1
         char_compare_stat2
         char_compare_stat3
         char_compare_stat4
         char_compare_stat5
         char_compare_stat6 $50;

  if  table_name in ('SYSTOLIC' 'DIASTOLIC') then do;
    NGAL_stat1  = ROUND(NGAL_stat1 , 1);
    NGAL_stat2  = ROUND(NGAL_stat2 , 1);
    NGAL_stat3  = ROUND(NGAL_stat3 , 1);
    NGAL_stat4  = ROUND(NGAL_stat4 , 1);
    NGAL_stat5  = ROUND(NGAL_stat5 , 1);
    NGAL_stat6  = ROUND(NGAL_stat6 , 1);
    NGAL_stat7  = ROUND(NGAL_stat7 , 1);
    NGAL_stat8  = ROUND(NGAL_stat8 , 1);
    NGAL_stat9  = ROUND(NGAL_stat9 , 1);
    NGAL_stat10 = ROUND(NGAL_stat10, 1);
    NGAL_stat11 = ROUND(NGAL_stat11, 1);
    NGAL_stat12 = ROUND(NGAL_stat12, 1);
    NGAL_stat13 = ROUND(NGAL_stat13, 1);
```

```
    NGAL_stat14 = ROUND(NGAL_stat14, 1);
    NGAL_stat15 = ROUND(NGAL_stat15, 1);
    NGAL_stat16 = ROUND(NGAL_stat16, 1);
    NGAL_stat17 = ROUND(NGAL_stat17, 1);
    NGAL_stat18 = ROUND(NGAL_stat18, 1);
  end;

  if category in ('count') and table_name in ('NGAL_CAT') then do;
         char_compare_stat1 = strip(put(NGAL_stat1,8.1)) ;
         char_compare_stat2 = strip(put(NGAL_stat4,8.1)) ;
         char_compare_stat3 = strip(put(NGAL_stat7,8.1)) ;
         char_compare_stat4 = strip(put(NGAL_stat10,8.1));
         char_compare_stat5 = strip(put(NGAL_stat13,8.1));
         char_compare_stat6 = strip(put(NGAL_stat16,8.1));
  end;
  else if category in ('mean') then do;
         char_compare_stat1 = strip(put(NGAL_stat1,8.1))  || " (" || strip(put(NGAL_stat2,8.1))
|| ")";
         char_compare_stat2 = strip(put(NGAL_stat4,8.1))  || " (" || strip(put(NGAL_stat5,8.1))
|| ")";
         char_compare_stat3 = strip(put(NGAL_stat7,8.1))  || " (" || strip(put(NGAL_stat8,8.1))
|| ")";
         char_compare_stat4 = strip(put(NGAL_stat10,8.1)) || " (" || strip(put(NGAL_stat11,8.1))
|| ")";
         char_compare_stat5 = strip(put(NGAL_stat13,8.1)) || " (" || strip(put(NGAL_stat14,8.1))
|| ")";
         char_compare_stat6 = strip(put(NGAL_stat16,8.1)) || " (" || strip(put(NGAL_stat17,8.1))
|| ")";
  end;
  else if category in ('count') then do;
         char_compare_stat1 = strip(put(NGAL_stat1,8.))  || " (" || strip(put(NGAL_stat2,8.1))
|| "%)";
         char_compare_stat2 = strip(put(NGAL_stat4,8.))  || " (" || strip(put(NGAL_stat5,8.1))
|| "%)";
         char_compare_stat3 = strip(put(NGAL_stat7,8.))  || " (" || strip(put(NGAL_stat8,8.1))
|| "%)";
         char_compare_stat4 = strip(put(NGAL_stat10,8.)) || " (" || strip(put(NGAL_stat11,8.1))
|| "%)";
         char_compare_stat5 = strip(put(NGAL_stat13,8.)) || " (" || strip(put(NGAL_stat14,8.1))
|| "%)";
         char_compare_stat6 = strip(put(NGAL_stat16,8.)) || " (" || strip(put(NGAL_stat17,8.1))
|| "%)";
  end;
  else if category in ('median') then do;
         char_compare_stat1 = strip(put(NGAL_stat1,8.1))  || " (" || strip(put(NGAL_stat2,8.1))
|| "," || strip(put(NGAL_stat3,8.1) || ")");
         char_compare_stat2 = strip(put(NGAL_stat4,8.1))  || " (" || strip(put(NGAL_stat5,8.1))
|| "," || strip(put(NGAL_stat6,8.1) || ")");
         char_compare_stat3 = strip(put(NGAL_stat7,8.1))  || " (" || strip(put(NGAL_stat8,8.1))
|| "," || strip(put(NGAL_stat9,8.1) || ")");
         char_compare_stat4 = strip(put(NGAL_stat10,8.1)) || " (" || strip(put(NGAL_stat11,8.1))
|| "," || strip(put(NGAL_stat12,8.1) || ")");
         char_compare_stat5 = strip(put(NGAL_stat13,8.1)) || " (" || strip(put(NGAL_stat14,8.1))
|| "," || strip(put(NGAL_stat15,8.1) || ")");
         char_compare_stat6 = strip(put(NGAL_stat16,8.1)) || " (" || strip(put(NGAL_stat17,8.1))
|| "," || strip(put(NGAL_stat18,8.1) || ")");
  end;

proc print data = compare_dataset;
  title3 'compare_dataset';

*** Importing the Table 1 Data taken from the primary outcome paper;
data table1_data;
  infile table1 delimiter = ',' MISSOVER DSD  firstobs=2 ls=1080;
  length characteristic $45 char_stat1-char_stat6 $23 category $12 table_name $ 30.;
  input
  characteristic $ table_name $ group category $ char_stat1 $      char_stat2 $   char_stat3 $
       char_stat4 $   char_stat5 $   char_stat6     $ stat1 stat2  stat3  stat4  stat5  stat6
       stat7  stat8  stat9  stat10 stat11 stat12 stat13 stat14 stat15 stat16 stat17 stat18
stat19 $
;
```

```
  if lengthn(characteristic) NE 0 then output table1_data;

data table1_data;
  set table1_data;
  sort_order = _n_;
  drop stat19;
  table_name = upcase(table_name);

proc print data = table1_data;
  title2 'table1_data';


*** Merging the DSIC Table 1 data and the Table 1 data from the manuscript;
*** Creating variables to calculate the difference between the datasets;
proc sort data = compare_dataset;
  by  table_name category group;
proc sort data = table1_data;
  by  table_name category group;

data combined_table1_dataset;
  merge compare_dataset (in = in1)
        table1_data     (in = in2)
        ;
  by table_name category group;
  if in1 and in2 then output combined_table1_dataset;
  else abort;

proc sort data = combined_table1_dataset;
  by sort_order;

*** Creating final character variables to show the comparison between DSIC and the Primary
Outcome Paper;
data combined_table1_dataset;
  set combined_table1_dataset;
  diff1   = round((stat1   -  NGAL_stat1 ), 0.1);
  diff2   = round((stat2   -  NGAL_stat2 ), 0.1);
  diff3   = round((stat3   -  NGAL_stat3 ), 0.1);
  diff4   = round((stat4   -  NGAL_stat4 ), 0.1);
  diff5   = round((stat5   -  NGAL_stat5 ), 0.1);
  diff6   = round((stat6   -  NGAL_stat6 ), 0.1);
  diff7   = round((stat7   -  NGAL_stat7 ), 0.1);
  diff8   = round((stat8   -  NGAL_stat8 ), 0.1);
  diff9   = round((stat9   -  NGAL_stat9 ), 0.1);
  diff10  = round((stat10  -  NGAL_stat10), 0.1);
  diff11  = round((stat11  -  NGAL_stat11), 0.1);
  diff12  = round((stat12  -  NGAL_stat12), 0.1);
  diff13  = round((stat13  -  NGAL_stat13), 0.1);
  diff14  = round((stat14  -  NGAL_stat14), 0.1);
  diff15  = round((stat15  -  NGAL_stat15), 0.1);
  diff16  = round((stat16  -  NGAL_stat16), 0.1);
  diff17  = round((stat17  -  NGAL_stat17), 0.1);
  diff18  = round((stat18  -  NGAL_stat18), 0.1);

  if category in ('median') then do;
          char_diff1 = strip(put(diff1,8.1))  || " (" || strip(put(diff2,8.1))  || "-" ||
strip(put(diff3,8.1) || ")");
          char_diff2 = strip(put(diff4,8.1))  || " (" || strip(put(diff5,8.1))  || "-" ||
strip(put(diff6,8.1) || ")");
          char_diff3 = strip(put(diff7,8.1))  || " (" || strip(put(diff8,8.1))  || "-" ||
strip(put(diff9,8.1) || ")");
          char_diff4 = strip(put(diff10,8.1)) || " (" || strip(put(diff11,8.1)) || "-" ||
strip(put(diff12,8.1) || ")");
          char_diff5 = strip(put(diff13,8.1)) || " (" || strip(put(diff14,8.1)) || "-" ||
strip(put(diff15,8.1) || ")");
          char_diff6 = strip(put(diff16,8.1)) || " (" || strip(put(diff17,8.1)) || "-" ||
strip(put(diff18,8.1) || ")");
  end;
  else if category in ('count') and strip(table_name) in ('NGAL_CAT') then do;
          char_diff1 = strip(put(diff1,8.)) ;
          char_diff2 = strip(put(diff4,8.)) ;
          char_diff3 = strip(put(diff7,8.)) ;
```

```
        char_diff4 = strip(put(diff10,8.)) ;
        char_diff5 = strip(put(diff13,8.)) ;
        char_diff6 = strip(put(diff16,8.)) ;
  end;
  else if category in ('count')  then do;
        char_diff1 = strip(put(diff1,8.))  || " (" || strip(put(diff2,8.1)) || "%)";
        char_diff2 = strip(put(diff4,8.))  || " (" || strip(put(diff5,8.1)) || "%)";
        char_diff3 = strip(put(diff7,8.))  || " (" || strip(put(diff8,8.1)) || "%)";
        char_diff4 = strip(put(diff10,8.)) || " (" || strip(put(diff11,8.1)) || "%)";
        char_diff5 = strip(put(diff13,8.)) || " (" || strip(put(diff14,8.1)) || "%)";
        char_diff6 = strip(put(diff16,8.)) || " (" || strip(put(diff17,8.1)) || "%)";
  end;
  else if category in ('mean') and strip(table_name) in ('SYSTOLIC' 'DIASTOLIC') then do;
        char_diff1 = strip(put(diff1,8.))  || " (" || strip(put(diff2,8.)) || "%)";
        char_diff2 = strip(put(diff4,8.))  || " (" || strip(put(diff5,8.)) || "%)";
        char_diff3 = strip(put(diff7,8.))  || " (" || strip(put(diff8,8.)) || "%)";
        char_diff4 = strip(put(diff10,8.)) || " (" || strip(put(diff11,8.)) || "%)";
        char_diff5 = strip(put(diff13,8.)) || " (" || strip(put(diff14,8.)) || "%)";
        char_diff6 = strip(put(diff16,8.)) || " (" || strip(put(diff17,8.)) || "%)";
  end;
  else if category in ('mean') then do;
        char_diff1 = strip(put(diff1,8.1))  || " (" || strip(put(diff2,8.1)) || "%)";
        char_diff2 = strip(put(diff4,8.1))  || " (" || strip(put(diff5,8.1)) || "%)";
        char_diff3 = strip(put(diff7,8.1))  || " (" || strip(put(diff8,8.1)) || "%)";
        char_diff4 = strip(put(diff10,8.1)) || " (" || strip(put(diff11,8.1)) || "%)";
        char_diff5 = strip(put(diff13,8.1)) || " (" || strip(put(diff14,8.1)) || "%)";
        char_diff6 = strip(put(diff16,8.1)) || " (" || strip(put(diff17,8.1)) || "%)";
  end;
  length characteristic_char $ 50.;
       if sort_order =  1  then characteristic_char = 'characteristic';
  else if sort_order =  2  then characteristic_char = 'Age,Mean (s.d.)
';
  else if sort_order =  3  then characteristic_char = 'sex Female                              ';
  else if sort_order =  4  then characteristic_char = 'race nonhispanic white
';
  else if sort_order =  5  then characteristic_char = 'race nonhispanic black
';
  else if sort_order =  6  then characteristic_char = 'race hispanic                            ';
  else if sort_order =  7  then characteristic_char = 'Diabetes                              ';
  else if sort_order =  8  then characteristic_char = '24-h proteinuria Mean (s.d.)
';
  else if sort_order =  9  then characteristic_char = '24-h proteinuria Median (IQR)
';
  else if sort_order = 10  then characteristic_char = 'Estimated GFR   Mean (s.d.)
';
  else if sort_order = 11  then characteristic_char = 'Estimated GFR   Median (IQR)
';
  else if sort_order = 12  then characteristic_char = 'Systolic BP    Mean (s.d.)
';
  else if sort_order = 13  then characteristic_char = 'Diastolic BP   Mean (s.d.)
';
  else if sort_order = 14  then characteristic_char = 'Body mass index  Mean (s.d.)
';
  else if sort_order = 15  then characteristic_char = 'History of cardiovascular disease';
  else if sort_order = 16  then characteristic_char = 'Use of ACE inhibitor or ARB      ';
     ;

proc freq data= combined_table1_dataset;
  tables char_diff1-char_diff6/list missing;

data combined_table1_dataset;
  set combined_table1_dataset;
   label
     char_stat1         = "<=6.9           [Manuscript]"
     char_compare_stat1 = "<=6.9           [DSIC]      "
     char_diff1         = "<=6.9           [Difference]"
     char_stat2         = ">6.9 to <=12.9  [Manuscript]"
     char_compare_stat2 = ">6.9 to <=12.9  [DSIC]      "
     char_diff2         = ">6.9 to <=12.9  [Difference]"
     char_stat3         = ">12.9 to <=22.6 [Manuscript]"
     char_compare_stat3 = ">12.9 to <=22.6 [DSIC]      "
```

```
     char_diff3         = ">12.9 to <=22.6 [Difference]"
     char_stat4         = ">22.6 to <=49.5 [Manuscript]"
     char_compare_stat4 = ">22.6 to <=49.5 [DSIC]      "
     char_diff4         = ">22.6 to <=49.5 [Difference]"
     char_stat5         = ">49.5 [Manuscript]          "
     char_compare_stat5 = ">49.5 [DSIC]                "
     char_diff5         = ">49.5 [Difference]          "
     char_stat6         = "ALL [Manuscript]            "
     char_compare_stat6 = "ALL [DSIC]                  "
     char_diff6         = "ALL [Difference]            "
;
run;
*** Outputting the dataset for table 1 to a csv file to be added to the DSIC;

ods listing close;

ods csv file = out_t1_b;
run;

proc print data = combined_table1_dataset NOOBS label;
       var characteristic_char
char_stat1
char_compare_stat1
char_stat2
char_compare_stat2
char_stat3
char_compare_stat3
;
run;
proc print data = combined_table1_dataset NOOBS label;
       var characteristic_char
char_stat4
char_compare_stat4
char_stat5
char_compare_stat5
char_stat6
char_compare_stat6
;
run;

ods csv close;
```

The FREQ Procedure

SurvAn ESRD/50% decline eGFR eGFR from MDRD

SA_ALLC_MDRD_RENAL1	Frequency	Percent	Cumulative Frequency	Cumulative Percent
0	1592	47.03	1592	47.03
1	882	26.06	2474	73.09
9	911	26.91	3385	100.00

NGAL_cat	case	Frequency	Percent	Cumulative Frequency	Cumulative Percent
1	0	640	18.91	640	18.91
1	1	40	1.18	680	20.09
2	0	600	17.73	1280	37.81
2	1	78	2.30	1358	40.12
3	0	569	16.81	1927	56.93
3	1	104	3.07	2031	60.00
4	0	510	15.07	2541	75.07
4	1	167	4.93	2708	80.00
5	0	389	11.49	3097	91.49
5	1	288	8.51	3385	100.00

NGAL_cat	SA_ALLC_DEATH	Frequency	Percent	Cumulative Frequency	Cumulative Percent
1	0	563	16.63	563	16.63
1	1	84	2.48	647	19.11
1	9	33	0.97	680	20.09
2	0	552	16.31	1232	36.40
2	1	86	2.54	1318	38.94
2	9	40	1.18	1358	40.12
3	0	535	15.81	1893	55.92
3	1	115	3.40	2008	59.32
3	9	23	0.68	2031	60.00
4	0	546	16.13	2577	76.13
4	1	88	2.60	2665	78.73
4	9	43	1.27	2708	80.00
5	0	502	14.83	3210	94.83
5	1	149	4.40	3359	99.23
5	9	26	0.77	3385	100.00

The FREQ Procedure

NGAL_cat	SA_ALLC_CRIC_RENAL1	Frequency	Percent	Cumulative Frequency	Cumulative Percent
1	0	364	10.75	364	10.75
1	1	73	2.16	437	12.91
1	9	243	7.18	680	20.09
2	0	300	8.86	980	28.95
2	1	116	3.43	1096	32.38
2	9	262	7.74	1358	40.12
3	0	280	8.27	1638	48.39
3	1	143	4.22	1781	52.61
3	9	250	7.39	2031	60.00
4	0	241	7.12	2272	67.12
4	1	222	6.56	2494	73.68
4	9	214	6.32	2708	80.00
5	0	165	4.87	2873	84.87
5	1	332	9.81	3205	94.68
5	9	180	5.32	3385	100.00

NGAL_cat	SA_ALLC_ESRD	Frequency	Percent	Cumulative Frequency	Cumulative Percent
1	0	536	15.83	536	15.83
1	1	40	1.18	576	17.02
1	2	72	2.13	648	19.14
1	9	32	0.95	680	20.09
2	0	494	14.59	1174	34.68
2	1	78	2.30	1252	36.99
2	2	72	2.13	1324	39.11
2	9	34	1.00	1358	40.12
3	0	464	13.71	1822	53.83
3	1	104	3.07	1926	56.90
3	2	85	2.51	2011	59.41
3	9	20	0.59	2031	60.00
4	0	420	12.41	2451	72.41
4	1	167	4.93	2618	77.34
4	2	59	1.74	2677	79.08
4	9	31	0.92	2708	80.00
5	0	291	8.60	2999	88.60
5	1	288	8.51	3287	97.10
5	2	79	2.33	3366	99.44
5	9	19	0.56	3385	100.00

The FREQ Procedure

SA_ALLC_ESRD	SA_ALLC_DEATH	NGAL_cat	Frequency	Percent	Cumulative Frequency	Cumulative Percent
0	0	1	536	15.83	536	15.83
0	0	2	494	14.59	1030	30.43
0	0	3	464	13.71	1494	44.14
0	0	4	420	12.41	1914	56.54
0	0	5	291	8.60	2205	65.14
1	0	1	27	0.80	2232	65.94
1	0	2	58	1.71	2290	67.65
1	0	3	71	2.10	2361	69.75
1	0	4	126	3.72	2487	73.47
1	0	5	211	6.23	2698	79.70
1	1	1	12	0.35	2710	80.06
1	1	2	14	0.41	2724	80.47
1	1	3	30	0.89	2754	81.36
1	1	4	29	0.86	2783	82.22
1	1	5	70	2.07	2853	84.28
1	9	1	1	0.03	2854	84.31
1	9	2	6	0.18	2860	84.49
1	9	3	3	0.09	2863	84.58
1	9	4	12	0.35	2875	84.93
1	9	5	7	0.21	2882	85.14
2	1	1	72	2.13	2954	87.27
2	1	2	72	2.13	3026	89.39
2	1	3	85	2.51	3111	91.91
2	1	4	59	1.74	3170	93.65
2	1	5	79	2.33	3249	95.98
9	9	1	32	0.95	3281	96.93
9	9	2	34	1.00	3315	97.93
9	9	3	20	0.59	3335	98.52
9	9	4	31	0.92	3366	99.44
9	9	5	19	0.56	3385	100.00

SA_ALLC_MDRD_RENAL1	SA_ALLC_CRIC_RENAL1	NGAL_cat	Frequency	Percent	Cumulative Frequency	Cumulative Percent
0	0	1	363	10.72	363	10.72
0	0	2	297	8.77	660	19.50
0	0	3	273	8.06	933	27.56
0	0	4	237	7.00	1170	34.56
0	0	5	162	4.79	1332	39.35
0	1	1	7	0.21	1339	39.56
0	1	2	3	0.09	1342	39.65
0	1	3	4	0.12	1346	39.76
0	1	4	3	0.09	1349	39.85
0	1	5	5	0.15	1354	40.00
0	9	1	54	1.60	1408	41.60
0	9	2	58	1.71	1466	43.31
0	9	3	62	1.83	1528	45.14
0	9	4	37	1.09	1565	46.23
0	9	5	27	0.80	1592	47.03
1	0	1	1	0.03	1593	47.06
1	0	2	3	0.09	1596	47.15
1	0	3	7	0.21	1603	47.36

The FREQ Procedure

SA_ALLC_MDRD_ RENAL1	SA_ALLC_CRIC_ RENAL1	NGAL_cat	Frequency	Percent	Cumulative Frequency	Cumulative Percent
1	0	4	4	0.12	1607	47.47
1	0	5	3	0.09	1610	47.56
1	1	1	65	1.92	1675	49.48
1	1	2	109	3.22	1784	52.70
1	1	3	139	4.11	1923	56.81
1	1	4	218	6.44	2141	63.25
1	1	5	324	9.57	2465	72.82
1	9	1	1	0.03	2466	72.85
1	9	2	2	0.06	2468	72.91
1	9	3	4	0.12	2472	73.03
1	9	4	1	0.03	2473	73.06
1	9	5	1	0.03	2474	73.09
9	1	1	1	0.03	2475	73.12
9	1	2	4	0.12	2479	73.23
9	1	4	1	0.03	2480	73.26
9	1	5	3	0.09	2483	73.35
9	9	1	188	5.55	2671	78.91
9	9	2	202	5.97	2873	84.87
9	9	3	184	5.44	3057	90.31
9	9	4	176	5.20	3233	95.51
9	9	5	152	4.49	3385	100.00

Frequency table of the NGAL_cat variable in the analysis dataset

The FREQ Procedure

Table of NGAL_cat by NGAL_cat

NGAL_cat NGAL_cat

Frequency Percent Row Pct Col Pct	1	2	3	4	5	Total
1	680 20.09 100.00 100.00	0 0.00 0.00 0.00	0 0.00 0.00 0.00	0 0.00 0.00 0.00	0 0.00 0.00 0.00	680 20.09
2	0 0.00 0.00 0.00	678 20.03 100.00 100.00	0 0.00 0.00 0.00	0 0.00 0.00 0.00	0 0.00 0.00 0.00	678 20.03
3	0 0.00 0.00 0.00	0 0.00 0.00 0.00	673 19.88 100.00 100.00	0 0.00 0.00 0.00	0 0.00 0.00 0.00	673 19.88
4	0 0.00 0.00 0.00	0 0.00 0.00 0.00	0 0.00 0.00 0.00	677 20.00 100.00 100.00	0 0.00 0.00 0.00	677 20.00
5	0 0.00 0.00 0.00	0 0.00 0.00 0.00	0 0.00 0.00 0.00	0 0.00 0.00 0.00	677 20.00 100.00 100.00	677 20.00
Total	680 20.09	678 20.03	673 19.88	677 20.00	677 20.00	3385 100.00

Frequency table of the SEX variable in the analysis dataset

The FREQ Procedure

Table of SEX by NGAL_cat

SEX(Sex (1=Male, 2=Female)) NGAL_cat

Frequency Percent Row Pct Col Pct	1	2	3	4	5	Total
1	577 17.05 32.18 84.85	420 12.41 23.42 61.95	292 8.63 16.29 43.39	233 6.88 12.99 34.42	271 8.01 15.11 40.03	1793 52.97
2	103 3.04 6.47 15.15	258 7.62 16.21 38.05	381 11.26 23.93 56.61	444 13.12 27.89 65.58	406 11.99 25.50 59.97	1592 47.03
Total	680 20.09	678 20.03	673 19.88	677 20.00	677 20.00	3385 100.00

Frequency table of the RACE_ETHNICITY_CAT2 variable in the analysis dataset

The FREQ Procedure

Table of RACE_ETHNICITY_CAT2 by NGAL_cat

RACE_ETHNICITY_CAT2(Race-Ethnicity Category (4-level))
NGAL_cat

Frequency / Percent / Row Pct / Col Pct	1	2	3	4	5	Total
1	396	331	263	240	180	1410
	11.70	9.78	7.77	7.09	5.32	41.65
	28.09	23.48	18.65	17.02	12.77	
	58.24	48.82	39.08	35.45	26.59	
2	205	277	314	332	311	1439
	6.06	8.18	9.28	9.81	9.19	42.51
	14.25	19.25	21.82	23.07	21.61	
	30.15	40.86	46.66	49.04	45.94	
3	40	43	76	83	162	404
	1.18	1.27	2.25	2.45	4.79	11.94
	9.90	10.64	18.81	20.54	40.10	
	5.88	6.34	11.29	12.26	23.93	
4	39	27	20	22	24	132
	1.15	0.80	0.59	0.65	0.71	3.90
	29.55	20.45	15.15	16.67	18.18	
	5.74	3.98	2.97	3.25	3.55	
Total	680	678	673	677	677	3385
	20.09	20.03	19.88	20.00	20.00	100.00

Frequency table of the Diabetes variable in the analysis dataset

The FREQ Procedure

Table of DIABETES by NGAL_cat

DIABETES(Diabetes) NGAL_cat

Frequency / Percent / Row Pct / Col Pct	1	2	3	4	5	Total
0	377	408	369	320	277	1751
	11.14	12.05	10.90	9.45	8.18	51.73
	21.53	23.30	21.07	18.28	15.82	
	55.44	60.18	54.83	47.27	40.92	
1	303	270	304	357	400	1634
	8.95	7.98	8.98	10.55	11.82	48.27
	18.54	16.52	18.60	21.85	24.48	
	44.56	39.82	45.17	52.73	59.08	
Total	680	678	673	677	677	3385
	20.09	20.03	19.88	20.00	20.00	100.00

Frequency table of the ANYCVD variable in the analysis dataset

The FREQ Procedure

Table of ANYCVD by NGAL_cat

ANYCVD(Cardio-Vascular Disease (Yes/Not Yes)) NGAL_cat

Frequency / Percent / Row Pct / Col Pct	1	2	3	4	5	Total
0	448	477	445	465	435	2270
	13.23	14.09	13.15	13.74	12.85	67.06
	19.74	21.01	19.60	20.48	19.16	
	65.88	70.35	66.12	68.69	64.25	
1	232	201	228	212	242	1115
	6.85	5.94	6.74	6.26	7.15	32.94
	20.81	18.03	20.45	19.01	21.70	
	34.12	29.65	33.88	31.31	35.75	
Total	680	678	673	677	677	3385
	20.09	20.03	19.88	20.00	20.00	100.00

Frequency table of the ACEARB variable in the analysis dataset

The FREQ Procedure

Table of ACEARB by NGAL_cat

ACEARB(Ace inhibitor or ARB) NGAL_cat

Frequency Percent Row Pct Col Pct	1	2	3	4	5	Total
0	178 5.29 16.50 26.33	205 6.10 19.00 30.46	219 6.51 20.30 32.69	236 7.02 21.87 35.07	241 7.17 22.34 35.97	1079 32.09
1	498 14.81 21.81 73.67	468 13.92 20.50 69.54	451 13.41 19.75 67.31	437 13.00 19.14 64.93	429 12.76 18.79 64.03	2283 67.91
Total	676 20.11	673 20.02	670 19.93	673 20.02	670 19.93	3362 100.00

Frequency Missing = 23

compare_freq

Obs	table_name	NGAL_stat1	NGAL_stat4	NGAL_stat7	NGAL_stat10	NGAL_stat13	NGAL_stat16	NGAL_stat2	NGAL_stat5	NGAL_stat8	NGAL_stat11	NGAL_stat14	NGAL_stat17	group	category
1	NGAL_cat	680	678	673	677	677	3385	.	.	.	.	.	.	.	count
2	SEX	103	258	381	444	406	1592	15.1	38.1	56.6	65.6	60.0	47.0	2	count
3	RACE_ETHNICITY_CAT2	396	331	263	240	180	1410	58.2	48.8	39.1	35.5	26.6	41.7	1	count
4	RACE_ETHNICITY_CAT2	205	277	314	332	311	1439	30.1	40.9	46.7	49.0	45.9	42.5	2	count
5	RACE_ETHNICITY_CAT2	40	43	76	83	162	404	5.9	6.3	11.3	12.3	23.9	11.9	3	count
6	Diabetes	303	270	304	357	400	1634	44.6	39.8	45.2	52.7	59.1	48.3	1	count
7	ANYCVD	232	201	228	212	242	1115	34.1	29.6	33.9	31.3	35.7	32.9	1	count
8	ACEARB	498	468	451	437	429	2283	73.7	69.5	67.3	64.9	64.0	67.9	1	count

compare_freq

NGAL_cat=1

The MEANS Procedure

Analysis Variable : AGE Participant Age

Mean	Std Dev	Median	25th Pctl	75th Pctl	Pr > |t|
58.6863127	10.3024697	60.7015720	53.4580695	65.8405981	<.0001

NGAL_cat=2

Analysis Variable : AGE Participant Age

Mean	Std Dev	Median	25th Pctl	75th Pctl	Pr > |t|
59.4298195	9.9802721	60.4945205	54.6896474	66.2986301	<.0001

NGAL_cat=3

Analysis Variable : AGE Participant Age

Mean	Std Dev	Median	25th Pctl	75th Pctl	Pr > |t|
59.5346198	10.8678910	61.6246575	54.2794521	67.6821918	<.0001

NGAL_cat=4

Analysis Variable : AGE Participant Age

Mean	Std Dev	Median	25th Pctl	75th Pctl	Pr > |t|
57.4837080	11.2782189	59.5205479	50.5104424	65.9123288	<.0001

NGAL_cat=5

Analysis Variable : AGE Participant Age

Mean	Std Dev	Median	25th Pctl	75th Pctl	Pr > |t|
56.1197977	11.9103962	57.6520548	49.5424658	65.1780822	<.0001

compare_freq

NGAL_cat=1

The MEANS Procedure

Analysis Variable : UPROTEIN24H 24H Urine Protein (g/24H)

Mean	Std Dev	Median	25th Pctl	75th Pctl	Pr > |t|
0.2886685	0.4458561	0.1020400	0.0666000	0.2700000	<.0001

NGAL_cat=2

Analysis Variable : UPROTEIN24H 24H Urine Protein (g/24H)

Mean	Std Dev	Median	25th Pctl	75th Pctl	Pr > |t|
0.4715859	0.8428731	0.1129057	0.0606000	0.4729513	<.0001

NGAL_cat=3

Analysis Variable : UPROTEIN24H 24H Urine Protein (g/24H)

Mean	Std Dev	Median	25th Pctl	75th Pctl	Pr > |t|
0.6717818	1.1127459	0.1601265	0.0694825	0.7358298	<.0001

NGAL_cat=4

Analysis Variable : UPROTEIN24H 24H Urine Protein (g/24H)

Mean	Std Dev	Median	25th Pctl	75th Pctl	Pr > |t|
1.1742029	1.7381893	0.2893800	0.0782015	1.6969392	<.0001

NGAL_cat=5

Analysis Variable : UPROTEIN24H 24H Urine Protein (g/24H)

Mean	Std Dev	Median	25th Pctl	75th Pctl	Pr > |t|
3.1048982	4.2622509	1.1375000	0.2269527	4.3612800	<.0001

compare_freq

NGAL_cat=1

The MEANS Procedure

Analysis Variable : EGFR_ROCHE Estimated Glomerular Filtration Rate (ml/min/1.73m2)

Mean	Std Dev	Median	25th Pctl	75th Pctl	Pr > |t|
47.9105937	12.0413744	48.0218806	39.4071445	56.0830348	<.0001

NGAL_cat=2

Analysis Variable : EGFR_ROCHE Estimated Glomerular Filtration Rate (ml/min/1.73m2)

Mean	Std Dev	Median	25th Pctl	75th Pctl	Pr > |t|
45.8778557	12.3883218	44.7479495	37.0848883	54.0689710	<.0001

NGAL_cat=3

Analysis Variable : EGFR_ROCHE Estimated Glomerular Filtration Rate (ml/min/1.73m2)

Mean	Std Dev	Median	25th Pctl	75th Pctl	Pr > |t|
42.2757821	12.7033118	41.1845969	33.0601333	50.7833321	<.0001

NGAL_cat=4

Analysis Variable : EGFR_ROCHE Estimated Glomerular Filtration Rate (ml/min/1.73m2)

Mean	Std Dev	Median	25th Pctl	75th Pctl	Pr > |t|
40.2151567	13.6372530	37.9540038	29.2190941	49.9083412	<.0001

NGAL_cat=5

Analysis Variable : EGFR_ROCHE Estimated Glomerular Filtration Rate (ml/min/1.73m2)

Mean	Std Dev	Median	25th Pctl	75th Pctl	Pr > |t|
35.6239787	13.4816961	33.7655347	25.0560905	43.5822759	<.0001

compare_freq

NGAL_cat=1

The MEANS Procedure

Analysis Variable : SYSTOLIC Systolic BP (mmHg)

Mean	Std Dev	Median	25th Pctl	75th Pctl	Pr > |t|
122.4702353	18.1653316	121.3300000	110.0000000	133.3300000	<.0001

NGAL_cat=2

Analysis Variable : SYSTOLIC Systolic BP (mmHg)

Mean	Std Dev	Median	25th Pctl	75th Pctl	Pr > |t|
125.6461062	19.4820433	124.0000000	112.0000000	137.3300000	<.0001

NGAL_cat=3

Analysis Variable : SYSTOLIC Systolic BP (mmHg)

Mean	Std Dev	Median	25th Pctl	75th Pctl	Pr > |t|
127.3131501	21.6553736	124.0000000	112.0000000	139.3300000	<.0001

NGAL_cat=4

Analysis Variable : SYSTOLIC Systolic BP (mmHg)

Mean	Std Dev	Median	25th Pctl	75th Pctl	Pr > |t|
130.7903693	22.9661590	128.0000000	114.0000000	145.3300000	<.0001

NGAL_cat=5

Analysis Variable : SYSTOLIC Systolic BP (mmHg)

Mean	Std Dev	Median	25th Pctl	75th Pctl	Pr > |t|
136.5082101	25.1006884	134.6700000	118.0000000	152.6700000	<.0001

compare_freq

NGAL_cat=1

The MEANS Procedure

Analysis Variable : DIASTOLIC Diastolic BP (mmHg)

Mean	Std Dev	Median	25th Pctl	75th Pctl	Pr > |t|
70.4608382	11.8712002	70.0000000	62.0000000	78.0000000	<.0001

NGAL_cat=2

Analysis Variable : DIASTOLIC Diastolic BP (mmHg)

Mean	Std Dev	Median	25th Pctl	75th Pctl	Pr > |t|
71.0918879	11.9176879	70.0000000	62.6700000	79.3300000	<.0001

NGAL_cat=3

Analysis Variable : DIASTOLIC Diastolic BP (mmHg)

Mean	Std Dev	Median	25th Pctl	75th Pctl	Pr > |t|
70.7345914	12.5892389	70.0000000	61.3300000	78.6700000	<.0001

NGAL_cat=4

Analysis Variable : DIASTOLIC Diastolic BP (mmHg)

Mean	Std Dev	Median	25th Pctl	75th Pctl	Pr > |t|
71.9192614	12.9500785	70.6700000	62.0000000	80.6700000	<.0001

NGAL_cat=5

Analysis Variable : DIASTOLIC Diastolic BP (mmHg)

Mean	Std Dev	Median	25th Pctl	75th Pctl	Pr > |t|
73.3239793	13.9257103	72.6700000	63.3300000	82.0000000	<.0001

compare_freq

NGAL_cat=1

The MEANS Procedure

Analysis Variable : BMI Body Mass Index (kg/m^2)

Mean	Std Dev	Median	25th Pctl	75th Pctl	Pr > |t|
31.1908858	6.7263965	30.2671579	26.9512226	34.3788781	<.0001

NGAL_cat=2

Analysis Variable : BMI Body Mass Index (kg/m^2)

Mean	Std Dev	Median	25th Pctl	75th Pctl	Pr > |t|
31.5729674	6.8757893	31.0249307	26.8280924	34.7934753	<.0001

NGAL_cat=3

Analysis Variable : BMI Body Mass Index (kg/m^2)

Mean	Std Dev	Median	25th Pctl	75th Pctl	Pr > |t|
32.3286651	7.8470215	31.3185915	26.8005951	36.3797693	<.0001

NGAL_cat=4

Analysis Variable : BMI Body Mass Index (kg/m^2)

Mean	Std Dev	Median	25th Pctl	75th Pctl	Pr > |t|
33.4550750	8.7594648	32.1775225	27.0860462	38.2059032	<.0001

NGAL_cat=5

Analysis Variable : BMI Body Mass Index (kg/m^2)

Mean	Std Dev	Median	25th Pctl	75th Pctl	Pr > |t|
32.5413406	8.9730209	30.7792481	26.1152883	37.6131428	<.0001

The MEANS Procedure

Analysis Variable : AGE Participant Age

Mean	Std Dev	Median	25th Pctl	75th Pctl	Pr > |t|
58.2500688	10.9588818	60.0000000	52.2876712	66.2986301	<.0001

The MEANS Procedure

Analysis Variable : UPROTEIN24H 24H Urine Protein (g/24H)

Mean	Std Dev	Median	25th Pctl	75th Pctl	Pr > |t|
1.1295311	2.3695938	0.1999184	0.0732288	0.9931489	<.0001

The MEANS Procedure

Analysis Variable : EGFR_ROCHE Estimated Glomerular Filtration Rate (ml/min/1.73m2)

Mean	Std Dev	Median	25th Pctl	75th Pctl	Pr > |t|
42.3867314	13.5635706	41.6149543	32.0542768	51.5100549	<.0001

The MEANS Procedure

Analysis Variable : SYSTOLIC Systolic BP (mmHg)

Mean	Std Dev	Median	25th Pctl	75th Pctl	Pr > |t|
128.5384752	22.1252885	126.0000000	112.6700000	141.3300000	<.0001

The MEANS Procedure

Analysis Variable : DIASTOLIC Diastolic BP (mmHg)

Mean	Std Dev	Median	25th Pctl	75th Pctl	Pr > |t|
71.5054374	12.7067635	70.6700000	62.0000000	80.0000000	<.0001

The MEANS Procedure

Analysis Variable : BMI Body Mass Index (kg/m^2)

Mean	Std Dev	Median	25th Pctl	75th Pctl	Pr > |t|
32.2157203	7.9237859	31.0879660	26.8122754	36.2185773	<.0001

Obs	table_name	NGAL_ stat1	NGAL_ stat4	NGAL_ stat7	NGAL_ stat10	NGAL_ stat13	NGAL_ stat16	NGAL_ stat2	NGAL_ stat5	NGAL_ stat8	NGAL_ stat11	NGAL_ stat14	NGAL_ stat17	group	category	NGAL_ stat3	NGAL_ stat6	NGAL_ stat9
1	NGAL_CAT	680.0	678.0	673.0	677.0	677.0	3385.0	.	.	.	.	.	.	.	count	.	.	.
2	SEX	103.0	258.0	381.0	444.0	406.0	1592.0	15.1	38.1	56.6	65.6	60.0	47.0	2	count	.	.	.
3	RACE_ETHNICITY_CAT2	396.0	331.0	263.0	240.0	180.0	1410.0	58.2	48.8	39.1	35.5	26.6	41.7	1	count	.	.	.
4	RACE_ETHNICITY_CAT2	205.0	277.0	314.0	332.0	311.0	1439.0	30.1	40.9	46.7	49.0	45.9	42.5	2	count	.	.	.
5	RACE_ETHNICITY_CAT2	40.0	43.0	76.0	83.0	162.0	404.0	5.9	6.3	11.3	12.3	23.9	11.9	3	count	.	.	.
6	DIABETES	303.0	270.0	304.0	357.0	400.0	1634.0	44.6	39.8	45.2	52.7	59.1	48.3	1	count	.	.	.
7	ANYCVD	232.0	201.0	228.0	212.0	242.0	1115.0	34.1	29.6	33.9	31.3	35.7	32.9	1	count	.	.	.
8	ACEARB	498.0	468.0	451.0	437.0	429.0	2283.0	73.7	69.5	67.3	64.9	64.0	67.9	1	count	.	.	.
9	BMI	31.2	31.6	32.3	33.5	32.5	32.2	6.7	6.9	7.8	8.8	9.0	7.9	.	mean	.	.	.
10	DIASTOLIC	71.0	71.0	71.0	72.0	73.0	72.0	12.0	12.0	13.0	13.0	14.0	13.0	.	mean	.	.	.
11	EGFR_ROCHE	47.9	45.9	42.3	40.2	35.6	42.4	12.0	12.4	12.7	13.6	13.5	13.6	.	mean	.	.	.
12	SYSTOLIC	123.0	126.0	127.0	131.0	137.0	129.0	18.0	20.0	22.0	23.0	25.0	22.0	.	mean	.	.	.
13	UPROTEIN24H	0.3	0.5	0.7	1.2	3.1	1.1	0.4	0.8	1.1	1.7	4.3	2.4	.	mean	.	.	.
14	AGE	58.7	59.4	59.5	57.5	56.1	58.3	10.3	10.0	10.9	11.3	11.9	11.0	.	mean	.	.	.
15	EGFR_ROCHE	48.0	44.7	41.2	38.0	33.8	41.6	39.4	37.1	33.1	29.2	25.1	32.1	.	median	56.1	54.1	50.8
16	UPROTEIN24H	0.1	0.1	0.2	0.3	1.1	0.2	0.1	0.1	0.1	0.1	0.2	0.1	.	median	0.3	0.5	0.7

Obs	NGAL_ stat12	NGAL_ stat15	NGAL_ stat18	char_compare_ stat1	char_compare_ stat2	char_compare_ stat3	char_compare_ stat4	char_compare_ stat5	char_compare_ stat6
1	.	.	.	680.0	678.0	673.0	677.0	677.0	3385.0
2	.	.	.	103 (15.1%)	258 (38.1%)	381 (56.6%)	444 (65.6%)	406 (60.0%)	1592 (47.0%)
3	.	.	.	396 (58.2%)	331 (48.8%)	263 (39.1%)	240 (35.5%)	180 (26.6%)	1410 (41.7%)
4	.	.	.	205 (30.1%)	277 (40.9%)	314 (46.7%)	332 (49.0%)	311 (45.9%)	1439 (42.5%)
5	.	.	.	40 (5.9%)	43 (6.3%)	76 (11.3%)	83 (12.3%)	162 (23.9%)	404 (11.9%)
6	.	.	.	303 (44.6%)	270 (39.8%)	304 (45.2%)	357 (52.7%)	400 (59.1%)	1634 (48.3%)
7	.	.	.	232 (34.1%)	201 (29.6%)	228 (33.9%)	212 (31.3%)	242 (35.7%)	1115 (32.9%)
8	.	.	.	498 (73.7%)	468 (69.5%)	451 (67.3%)	437 (64.9%)	429 (64.0%)	2283 (67.9%)
9	.	.	.	31.2 (6.7)	31.6 (6.9)	32.3 (7.8)	33.5 (8.8)	32.5 (9.0)	32.2 (7.9)
10	.	.	.	71.0 (12.0)	71.0 (12.0)	71.0 (13.0)	72.0 (13.0)	73.0 (14.0)	72.0 (13.0)
11	.	.	.	47.9 (12.0)	45.9 (12.4)	42.3 (12.7)	40.2 (13.6)	35.6 (13.5)	42.4 (13.6)
12	.	.	.	123.0 (18.0)	126.0 (20.0)	127.0 (22.0)	131.0 (23.0)	137.0 (25.0)	129.0 (22.0)
13	.	.	.	0.3 (0.4)	0.5 (0.8)	0.7 (1.1)	1.2 (1.7)	3.1 (4.3)	1.1 (2.4)
14	.	.	.	58.7 (10.3)	59.4 (10.0)	59.5 (10.9)	57.5 (11.3)	56.1 (11.9)	58.3 (11.0)
15	49.9	43.6	51.5	48.0 (39.4,56.1)	44.7 (37.1,54.1)	41.2 (33.1,50.8)	38.0 (29.2,49.9)	33.8 (25.1,43.6)	41.6 (32.1,51.5)
16	1.7	4.4	1.0	0.1 (0.1,0.3)	0.1 (0.1,0.5)	0.2 (0.1,0.7)	0.3 (0.1,1.7)	1.1 (0.2,4.4)	0.2 (0.1,1.0)

table1_data

Obs	characteristic	char_stat1	char_stat2	char_stat3	char_stat4
1	NGAL_cat	681	678	673	677
2	Age	58.7 (10.3)	59.4 (10.0)	59.5 (10.9)	57.5 (11.3)
3	sex	103 (15.1%)	258 (38.1%)	381 (56.6%)	444 (65.6%)
4	race	396 (58.1%)	331 (48.8%)	263 (39.1%)	240 (35.5%)
5	race	206 (30.2%)	277 (40.9%)	314 (46.7%)	332 (49.0%)
6	race	40 (5.9%)	43 (6.3%)	76 (11.3%)	83 (12.3%)
7	Diabetes	303 (44.5%)	270 (39.8%)	304 (45.2%)	357 (52.7%)
8	24-h proteinuria	0.3 (0.4)	0.5 (0.8)	0.7 (1.1)	1.2 (1.7)
9	24-h proteinuria	0.1 (0.1,0.3)	0.1 (0.1,0.5)	0.2 (0.1,0.7)	0.3 (0.1,1.7)
10	Estimated GFR	47.9 (12.0)	45.9 (12.4)	42.3 (12.7)	40.2 (13.6)
11	Estimated GFR	48.0 (39.5,56.1)	44.7 (37.1,54.1)	41.2 (33.1,50.8)	38.0 (29.2,49.9)
12	Systolic BP	123 (18)	126 (20)	127 (22)	131 (23)
13	Diastolic BP	71 (12)	71 (12)	71 (13)	72(13)
14	Body mass index	31.2 (6.7)	31.6 (6.9)	32.3 (7.8)	33.5 (8.8)
15	History of cardiovascular disease	233 (34.2%)	201 (29.6%)	228 (33.9%)	212 (31.3%)

Obs	char_stat5	char_stat6	category	table_name	group	stat1	stat2	stat3	stat4	stat5
1	677	3386	count	NGAL_CAT	.	681.0	.	.	678.0	.
2	56.1 (11.9)	58.2 (11.0)	mean	AGE	.	58.7	10.3	.	59.4	10.0
3	406 (60.0%)	1592 (47.0%)	count	SEX	2	103.0	15.1	.	258.0	38.1
4	180 (26.6%)	1410 (41.6%)	count	RACE_ETHNICITY_CAT2	1	396.0	58.1	.	331.0	48.8
5	311 (45.9%)	1440 (42.5%)	count	RACE_ETHNICITY_CAT2	2	206.0	30.2	.	277.0	40.9
6	162 (23.9%)	404 (11.9%)	count	RACE_ETHNICITY_CAT2	3	40.0	5.9	.	43.0	6.3
7	400 (59.1%)	1634 (48.3%)	count	DIABETES	1	303.0	44.5	.	270.0	39.8
8	3.1 (4.3)	1.1 (2.4)	mean	UPROTEIN24H	.	0.3	0.4	.	0.5	0.8
9	1.1 (0.2,4.4)	0.2 (0.1,1.0)	median	UPROTEIN24H	.	0.1	0.1	0.3	0.1	0.1
10	35.6 (13.5)	42.4 (13.6)	mean	EGFR_ROCHE	.	47.9	12.0	.	45.9	12.4
11	33.8 (25.1,43.6)	41.6 (32.1,51.5)	median	EGFR_ROCHE	.	48.0	39.5	56.1	44.7	37.1
12	137 (25)	129 (22)	mean	SYSTOLIC	.	123.0	18.0	.	126.0	20.0
13	73 (14)	72(13)	mean	DIASTOLIC	.	71.0	12.0	.	71.0	12.0
14	32.5 (9.0)	32.2 (7.9)	mean	BMI	.	31.2	6.7	.	31.6	6.9
15	242 (35.7%)	1116 (33.0%)	count	ANYCVD	1	233.0	34.2	.	201.0	29.6

Obs	stat6	stat7	stat8	stat9	stat10	stat11	stat12	stat13	stat14	stat15	stat16	stat17	stat18	sort_order
1	.	673.0	.	.	677.0	.	.	677.0	.	.	3386.0	.	.	1
2	.	59.5	10.9	.	57.5	11.3	.	56.1	11.9	.	58.2	11.0	.	2
3	.	381.0	56.6	.	444.0	65.6	.	406.0	60.0	.	1592.0	47.0	.	3
4	.	263.0	39.1	.	240.0	35.5	.	180.0	26.6	.	1410.0	41.6	.	4
5	.	314.0	46.7	.	332.0	49.0	.	311.0	45.9	.	1440.0	42.5	.	5
6	.	76.0	11.3	.	83.0	12.3	.	162.0	23.9	.	404.0	11.9	.	6
7	.	304.0	45.2	.	357.0	52.7	.	400.0	59.1	.	1634.0	48.3	.	7
8	.	0.7	1.1	.	1.2	1.7	.	3.1	4.3	.	1.1	2.4	.	8
9	0.5	0.2	0.1	0.7	0.3	0.1	1.7	1.1	0.2	4.4	0.2	0.1	1.0	9
10	.	42.3	12.7	.	40.2	13.6	.	35.6	13.5	.	42.4	13.6	.	10
11	54.1	41.2	33.1	50.8	38.0	29.2	49.9	33.8	25.1	43.6	41.6	32.1	51.5	11
12	.	127.0	22.0	.	131.0	23.0	.	137.0	25.0	.	129.0	22.0	.	12
13	.	71.0	13.0	.	72.0	13.0	.	73.0	14.0	.	72.0	13.0	.	13
14	.	32.3	7.8	.	33.5	8.8	.	32.5	9.0	.	32.2	7.9	.	14
15	.	228.0	33.9	.	212.0	31.3	.	242.0	35.7	.	1116.0	33.0	.	15

table1_data

Obs	characteristic	char_stat1	char_stat2	char_stat3	char_stat4
16	Use of ACE inhibitor or ARB	499 (73.7%)	468 (69.5%)	451 (67.3%)	437 (64.9%)

Obs	char_stat5	char_stat6	category	table_name	group	stat1	stat2	stat3	stat4	stat5
16	429 (64.0%)	2284 (67.9%)	count	ACEARB	1	499.0	73.7	.	468.0	69.5

Obs	stat6	stat7	stat8	stat9	stat10	stat11	stat12	stat13	stat14	stat15	stat16	stat17	stat18	sort_ order
16	.	451.0	67.3	.	437.0	64.9	.	429.0	64.0	.	2284.0	67.9	.	16

table1_data

The FREQ Procedure

char_diff1	Frequency	Percent	Cumulative Frequency	Cumulative Percent
0 (-0.1%)	2	12.50	2	12.50
0 (0%)	2	12.50	4	25.00
0 (0.0%)	2	12.50	6	37.50
0.0 (0.0%)	4	25.00	10	62.50
0.0 (0.0-0.0)	1	6.25	11	68.75
0.0 (0.1-0.0)	1	6.25	12	75.00
1	1	6.25	13	81.25
1 (0.0%)	1	6.25	14	87.50
1 (0.1%)	2	12.50	16	100.00

char_diff2	Frequency	Percent	Cumulative Frequency	Cumulative Percent
0	1	6.25	1	6.25
0 (0%)	2	12.50	3	18.75
0 (0.0%)	7	43.75	10	62.50
0.0 (0.0%)	4	25.00	14	87.50
0.0 (0.0-0.0)	2	12.50	16	100.00

char_diff3	Frequency	Percent	Cumulative Frequency	Cumulative Percent
0	1	6.25	1	6.25
0 (0%)	2	12.50	3	18.75
0 (0.0%)	7	43.75	10	62.50
0.0 (0.0%)	4	25.00	14	87.50
0.0 (0.0-0.0)	2	12.50	16	100.00

char_diff4	Frequency	Percent	Cumulative Frequency	Cumulative Percent
0	1	6.25	1	6.25
0 (0%)	2	12.50	3	18.75
0 (0.0%)	7	43.75	10	62.50
0.0 (0.0%)	4	25.00	14	87.50
0.0 (0.0-0.0)	2	12.50	16	100.00

char_diff5	Frequency	Percent	Cumulative Frequency	Cumulative Percent
0	1	6.25	1	6.25
0 (0%)	2	12.50	3	18.75
0 (0.0%)	7	43.75	10	62.50
0.0 (0.0%)	4	25.00	14	87.50
0.0 (0.0-0.0)	2	12.50	16	100.00

table1_data

The FREQ Procedure

char_diff6	Frequency	Percent	Cumulative Frequency	Cumulative Percent
-0.1 (0.0%)	1	6.25	1	6.25
0 (-0.1%)	1	6.25	2	12.50
0 (0%)	2	12.50	4	25.00
0 (0.0%)	3	18.75	7	43.75
0.0 (0.0%)	3	18.75	10	62.50
0.0 (0.0-0.0)	2	12.50	12	75.00
1	1	6.25	13	81.25
1 (0.0%)	2	12.50	15	93.75
1 (0.1%)	1	6.25	16	100.00