

```

%_mprintto;
options notes nosource;
proc datasets lib=work nolist memtype=data kill; quit;
%put NOTE:
=====;
%put NOTE: Covance Study Number : 0000001063264;
%put NOTE: Client Protocol ID   : ZRHR-REXC-03-EU;
%put NOTE: Program Name        : t_pbio.sas;
%put NOTE: Purpose              : table of primary biomarkers and change
from baseline on Day 5 ;
%put NOTE: ;
%put NOTE: Input Data           : ADAM.ADBX ADAM.ADSL;
%put NOTE: Output               : t_15_2_3_5(pbio);
%put NOTE: Macros Called        : _MPRINTTO;
%put NOTE: ;
%put NOTE: Programmed by        : cvn_smulholl;
%put NOTE: Creation Date        : 2014-05-14;
%put NOTE: SAS Version          : 9.3;
%put NOTE: ;
%put NOTE: == Latest Run
=====;
%put NOTE: Run by                : &sysuserid;
%put NOTE: Date/Time             :
%sysfunc(putn(%sysfunc(date()),e8601da.))T%sysfunc(putn(%sysfunc(time()),
e86011z.));
%put NOTE: ;
%put NOTE: == Modification History
=====;
%put NOTE: Date      Initials  No. Reason;
%put NOTE: 15May2014    SM      1)  Exclude absolute data and amend
titles, variables labels etc to match;
%put NOTE:                                2)  Amend format of pchg to ldp for
all;
%put NOTE: 11Jun2014   JMH      3)  Amended er-ror with merge and added
BLQ footnoes;
%put NOTE: 19Jun2014   JMH      4)  Amended parameter names to match
figures;
%put NOTE: 19Jun2014   JMH      5)  Amneded BLQ footnote;
%put NOTE: 23Jun2014   JMH      6)  Amended in line with ADBX updates;
%put NOTE: 24Jun2014   JMH      7)  Amended in line with format
updates;
%put NOTE: 01Aug2014   JMH      8)  Amended in line with format
updates;
%put NOTE: 05Aug2014   JMH      9)  Removed BLOQ counts for COHb;
%put NOTE: 18Sep2014   JR      10) Updated baseline footnote;
%put NOTE: 25Sep2014   JR      11) Amended calculation of bloq;
%put NOTE: 02Oct2014   JMH      12) Added in BLOQ count for COHb;
%put NOTE: ;
%put NOTE: ;
%put NOTE:
=====;
options notes source source2 nofullstimer validvarname=upcase missing='
';
ods _all_ close;

```

```

ods listing;

*=====;
* START OF PROGRAM CODE                                     ;
*=====;

%let tflno=T_15_02_03_05(pbio);

%let TFL_Part=%scan(&_SASPROGRAMFILE,-3,%str(/));

data _null_;
    tmp="%TFL_Part";
    if tmp not in ("dev" "qc") then call symput("TFL_Part", "prod");
    call symput('TFLpath', compress("&_SASPROGRAMFILE",""));
run;

*****;
* read in data ;
*****;

/*Use ADSL to get N values for column headers*/
data adsl;
    set adam.adsl(where=(fasfl='Y'));
run;

proc sort data=adsl nodupkey out=adsl1;
    by trt01an trt01a subjid;
run;

proc freq data=adsl1(where=(not missing(trt01an))) noprint;
    table trt01an*trt01a/ out =tot(drop=percent rename=(count=total));
run;

data tot2;
    set tot;
    call symput('trt' || compress(put(trt01an,best.)),
compress(total));
run;

/*Bring in appropriate data from ADBX*/
data adbx1;
    set adam.adbx(where=(anl02fl='Y' and fasfl='Y' and avisit='Day 5'
and paramcd in ('CARBXHGB' 'UMHBMCRE' 'U3HPMCRE' 'USPMACRE')));
    /*if paramcd='U3HPMCRE' then paramn=paramn+30;*/ * move up order for
output;
    if paramcd='CARBXHGB' and atpt ne '08:00-10:00 PM' then delete; *
specific time point required;
run;

data adbx;
    set adbx1;
run;

data adbx_orig;

```

```

        set adbx;
        statval=aval;
        type='abs';
        output;
        statval=pchg;
        type='pchg';
        output;
run;

proc sort data=adbx_orig;
    by paramn param type trtan trta AVALU; /* 6) JMH 23Jun2014 */
run;

proc means data=adbx_orig noprint;
    var statval;
    by paramn param type trtan trta AVALU; /* 6) JMH 23Jun2014 */
    output out=results02 n=n1 mean=mean1 std=std1 median=median1 min=min1
max=max1 q1=q1 q3=q3 lclm=lci1 uclm=uci1;
run;

data results03;
    set results02;
    attrib meansd length=$20.
            minmax length=$20.
            n      length=$20.
            median length=$20.
            quart  ci length=$20.;

    n = left(compress(put(n1,8.)));
    * differing DP per biomarker ;
    IF TYPE='ABS' THEN DO; /* 2) SM 15May2014 */

/* 7) start JMH 24Jun2014 */
/*if paramn=50 then do;*/ * 3-HPMA as integer;
/*    if not missing(median1) then median =
left(compress(put(median1,8.1))); */
/*    if not missing(mean1) and not missing(std1) then meansd =
left(compress(put(mean1,8.1))) || ' (' ||
left(compress(put(0.01*ceil(std1/0.01),8.2))) || ')'; */
/*    if not missing(min1) and not missing(max1) then minmax =
left(compress(put(min1,8.))) || ', ' || left(compress(put(max1,8.)));*/
/*    if not missing(lci1) and not missing(uci1) then ci =
strip(put(0.1*floor(lci1/0.1),8.1)) || ', ' ||
strip(put(0.1*ceil(uci1/0.1),8.1)); */
/*    if not missing(q1) and not missing(q3) then quart =
strip(strip(put(0.1*FLOOR(q1/0.1),8.1)) || ', ' ||
strip(put(0.1*CEIL(q3/0.1),8.1))); /* 7) JMH 24Jun2014 */ */
/*    end;*/
    else if paramn=2 then do; * COHb as ldp;
        if not missing(median1) then median =
left(compress(put(ROUND(median1,0.01),8.2)));

```

```

        if not missing(mean1) and not missing(std1) then meansd =
left(compress(put(ROUND(mean1,0.01),8.2))) || ' (' ||
left(compress(put(0.001*ceil(std1/0.001),8.3))) || ')';
        if not missing(min1) and not missing(max1) then minmax =
left(compress(put(ROUND(min1,0.1),8.1))) || ', ' ||
left(compress(put(ROUND(max1,0.1),8.1)));
        if not missing(lcil) and not missing(ucil) then ci =
strip(put(0.01*floor(lcil/0.01),8.2)) || ', ' ||
strip(put(0.01*ceil(ucil/0.01),8.2));
        if not missing(q1) and not missing(q3) then quart =
strip(strip(put(0.01*FLOOR(q1/0.01),8.2)) || ', ' ||
strip(put(0.01*CEIL(q3/0.01),8.2)));
/*      end;*/
        /*else if paramn=44 then do;*/ * MHBMA as 3dp;
/*      if not missing(median1) then median =
left(compress(put(median1,8.4))); */
/*      if not missing(mean1) and not missing(std1) then meansd =
left(compress(put(mean1,8.4))) || ' (' ||
left(compress(put(0.00001*ceil(std1/0.00001),8.5))) || ')'; */
/*      if not missing(min1) and not missing(max1) then minmax =
left(compress(put(min1,8.3))) || ', ' || left(compress(put(max1,8.3)));*/
/*      if not missing(lcil) and not missing(ucil) then ci =
strip(put(0.0001*floor(lcil/0.0001),8.4)) || ', ' ||
strip(put(0.0001*ceil(ucil/0.0001),8.4)); */
/*      if not missing(q1) and not missing(q3) then quart =
strip(strip(put(0.0001*FLOOR(q1/0.0001),8.4)) || ', ' ||
strip(put(0.0001*CEIL(q3/0.0001),8.4))); */
/*      end;*/
        /*else if paramn=63 then do;*/ * SPMA as 4dp;
/*      if not missing(median1) then median =
left(compress(put(median1,8.5))); */
/*      if not missing(mean1) and not missing(std1) then meansd =
left(compress(put(mean1,8.5))) || ' (' ||
left(compress(put(0.000001*ceil(std1/0.000001),8.6))) || ')'; */
/*      if not missing(min1) and not missing(max1) then minmax =
left(compress(put(min1,8.4))) || ', ' || left(compress(put(max1,8.4)));*/
/*      if not missing(lcil) and not missing(ucil) then ci =
strip(put(0.00001*floor(lcil/0.00001),8.5)) || ', ' ||
strip(put(0.00001*ceil(ucil/0.00001),8.5)); */
/*      if not missing(q1) and not missing(q3) then quart =
strip(strip(put(0.00001*FLOOR(q1/0.00001),8.5)) || ', ' ||
strip(put(0.00001*CEIL(q3/0.00001),8.5))); */
/*      end;*/
END; /* 2) SM 15May2014 */
ELSE DO; /* new section 2) SM 15May2014 */
        if not missing(median1) then median =
left(compress(put(ROUND(median1,0.01),8.2)));
        if not missing(mean1) and not missing(std1) then meansd =
left(compress(put(ROUND(mean1,0.01),8.2))) || ' (' ||
left(compress(put(0.001*ceil(std1/0.001),8.3))) || ')';
        if not missing(min1) and not missing(max1) then minmax =
left(compress(put(ROUND(min1,0.1),8.1))) || ', ' ||
left(compress(put(ROUND(max1,0.1),8.1)));

```

```

        if not missing(lcil) and not missing(ucil) then ci =
strip(put(0.01*floor(lcil/0.01),8.2)) || ', ' ||
strip(put(0.01*ceil(ucil/0.01),8.2));
        if not missing(q1) and not missing(q3) then quart =
strip(strip(put(0.01*FLOOR(q1/0.01),8.2)) || ', ' ||
strip(put(0.01*CEIL(q3/0.01),8.2)));
        END;
        drop /*n1*/ mean1 std1 median1 min1 max1 q1 q3 ucil lcil ; /* 11) JR
25Sep2014 */
run;

```

```

/*Obtain subjects with values BLOQ*/

```

```

data adbx_blq;

```

```

    set adbx;

```

```

    where bloqfl='Y';

```

```

    statval=aval;

```

```

    type='abs';

```

```

    output;

```

```

    statval=pchg;

```

```

    type='pch';

```

```

    output;

```

```

run;

```

```

proc freq data=adbx_blq noprint;

```

```

    table paramn*param*type*trtan*trta/ out =blq(drop=percent);

```

```

run;

```

```

%macro outrtf(blankn=, halfblnk=);

```

```

%if &halfblnk=N %then %let halfblnk=;

```

```

%else %if &halfblnk=Y %then %let halfblnk=~;

```

```

%let dsid=%sysfunc(open(blq));

```

```

%let nsum=%sysfunc(attrn(&dsid.,nobs));

```

```

%let rc=%sysfunc(close(&dsid.));

```

```

%put "Check " &nsum.;

```

```

%if &nsum. lt 1 %then %do;

```

```

    proc sort data=adbx nodupkey out=tpts(keep=paramn param trtan
trta);

```

```

        by paramn param trtan trta;

```

```

    run;

```

```

    data blq1;

```

```

        set tpts;

```

```

        attrib blq length=$50.;

```

```

        blq='0';

```

```

    run;

```

```

%end;

```

```

%else %do;
  /* 3) start JMH 11Jun2014 */
  /*DATA ADSL_BLO_ABS;*/
  /* SET TOT;*/
  /* ATTRIB PARAM LENGTH=$200.*/
  /* PARAMN LENGTH=8.*/
  /* TYPE LENGTH=$3.;*/
  /* RENAME TRT01AN=TRTAN;*/
  /* RENAME TRT01A=TRTA;*/
  /* TYPE='abs';*/
  /**/
  /* PARAMN=2;*/
  /* PARAM='Carboxyhemoglobin (%)';*/
  /* OUTPUT;*/
  /*PARAMN=4544;*/ /* 6) JMH 23Jun2014 */
  /* PARAM='Monohydroxybutenyl Mercapturic Acid (ng/mg
creat)' 'Monohydroxybutenyl Mercapturic Acid (pg/mg creat)';*/ /* 6) JMH
23Jun2014 */
  /* OUTPUT;*/
  /* PARAMN=1950;*/ /* 6) JMH 23Jun2014 */
  /* PARAM='3-hydroxypropylmercaptopuric Acid (ng/mg creat)';*/
  /* OUTPUT;*/
  /* PARAMN=6663;*/ /* 6) JMH 23Jun2014 */
  /*PARAM='S-phenylmercaptopuric Acid (ng/mg creat)' 'S-
phenylmercaptopuric Acid (pg/mg creat)';*/ /* 6) JMH 23Jun2014 */
  /* OUTPUT;*/
  /*RUN;*/
  /**/
  /*DATA ADSL_BLO_PCH;*/
  /* SET TOT;*/
  /* ATTRIB PARAM LENGTH=$200.*/
  /* PARAMN LENGTH=8.*/
  /* TYPE LENGTH=$3.;*/
  /* RENAME TRT01AN=TRTAN;*/
  /* RENAME TRT01A=TRTA;*/
  /* TYPE='pch';*/
  /**/
  /* PARAMN=2;*/
  /* PARAM='Carboxyhemoglobin (%)';*/
  /* OUTPUT;*/
  /* PARAMN=4544;*/ /* 6) JMH 23Jun2014 */
  /* PARAM='Monohydroxybutenyl Mercapturic Acid (ng/mg
creat)' 'Monohydroxybutenyl Mercapturic Acid (pg/mg creat)';*/ /* 6) JMH
23Jun2014 */
  /* OUTPUT;*/
  /* PARAMN=19; 6) JMH 23Jun2014 */
  /* PARAM='3-hydroxypropylmercaptopuric Acid (ng/mg creat)';*/
  /* OUTPUT;*/
  /*PARAMN=6663;*/ /* 6) JMH 23Jun2014 */
  /*PARAM='S-phenylmercaptopuric Acid (ng/mg creat)' 'S-
phenylmercaptopuric Acid (pg/mg creat)';*/ /* 6) JMH 23Jun2014 */
  /* OUTPUT;*/
  /*RUN;*/

```

```

/**/
/*PROC SORT DATA=ADSL_BLO_ABS; BY TYPE TRTAN TRTA PARAMN PARAM; RUN;*/
/*PROC SORT DATA=ADSL_BLO_PCH; BY TYPE TRTAN TRTA PARAMN PARAM; RUN;*/
/**/
/*DATA ADSL_BLO;*/
/*    MERGE ADSL_BLO_ABS ADSL_BLO_PCH;*/
/*    BY TYPE TRTAN TRTA PARAMN PARAM;*/
/*RUN;*/
/**/
/*PROC SORT DATA=ADSL_BLO; BY TRTAN TRTA; RUN;*/
/**/
/*DATA TOT3;*/
/*    SET TOT;*/
/*    RENAME TRT01AN=TRTAN;*/
/*    RENAME TRT01A=TRTA;*/
/*RUN;*/
/**/
/*DATA TOT_BLO;*/
/*    MERGE ADSL_BLO(IN=A) TOT3(IN=B);*/
/*    BY TRTAN TRTA;*/
/*RUN;*/
/**/
/*PROC SORT DATA=BLO; BY TRTAN TRTA TYPE PARAMN PARAM; RUN;*/
/*PROC SORT DATA=TOT_BLO; BY TRTAN TRTA TYPE PARAMN PARAM; RUN;*/
/* 3) end JMH 11Jun2014 */
/* start 11) JR 25Sep2014 */
    PROC SORT DATA=ADBX_ORIG NODUPKEY OUT=TPTS(KEEP=TYPE PARAMN PARAM
TRTAN TRTA);
        BY TRTAN TRTA TYPE PARAMN PARAM;
    RUN;

    DATA BLQTOTS;
        SET RESULTS03(RENAME=(N1=TOTAL));
        KEEP TYPE TR: PARAMN PARAM TOTAL;
    RUN;

    PROC SORT DATA=BLQTOTS; BY TRTAN TRTA TYPE PARAMN PARAM; RUN;
    PROC SORT DATA=TPTS; BY TRTAN TRTA TYPE PARAMN PARAM; RUN;

    DATA TOT_BLO;
        MERGE TPTS BLQTOTS;
        BY TRTAN TRTA TYPE PARAMN PARAM;
    RUN;

    PROC SORT DATA=TOT_BLO;
        BY TRTAN TRTA TYPE PARAMN PARAM;
    RUN;

    PROC SORT DATA=BLO;
        BY TRTAN TRTA TYPE PARAMN PARAM;
    RUN;
/* end 11) JR 25Sep2014 */
    data blq1;
        attrib blq length=$50.;

```

```

merge blq(in=a) tot_BLQ(IN=B); /* 3) JMH 11Jun2014 */
by trtan trta TYPE paramn PARAMN PARAM; /* 3) JMH
11Jun2014 */
    if not a then do;
        count=0;
    end;
    IF TOTAL NE 0 THEN percent1=count/total*100; /* 11) JR
25Sep2014 */
    ELSE PERCENT = 0; /* 11) JR 25Sep2014 */
    PERCENT=ROUND(PERCENT1,0.1); /* 3) JMH 11Jun2014 */

    if count=0 then blq='0';
    else if percent=100 then blq= put(count,3.)||' (100%)';
    else blq=put(count,3.)||'
('||put(percent,5.1/*3.*/)||'%)'; /* 3) JMH 11Jun2014 */
        run;
%end;

proc sort data=results03;
    by trtan trta TYPE paramn PARAM ; /* 3) JMH 11Jun2014 */ /* 6) JMH
23Jun2014 */
run;

proc sort data=blq1;
    by trtan trta TYPE paramn PARAM; /* 3) JMH 11Jun2014 */ /* 6) JMH
23Jun2014 */
run;

data results04;
    merge results03 blq1;
    by trtan trta TYPE paramn PARAM ; /* 3) JMH 11Jun2014 */ /* 6) JMH
23Jun2014 */
run;

proc sort data=results04;
    by paramn param type AVALU; /* 6) JMH 23Jun2014 */
run;

proc transpose data=results04 out=results05 prefix=_ name=varname;
    by paramn param type AVALU; /* 6) JMH 23Jun2014 */
    var n meansd median minmax ci quart blq;
    id trtan;
    idlabel trta;
run;

data results06;
    set results05;
    attrib stat variable length = $100.;

    if type='pch'/'abs'*/ then do; /* 1) SM 15May2014 */
        if paramn=2 then variable='Evening COHb (%)';
/*         else variable=trim(param);*/

```



```

        ELSE IF PARAMN=19 THEN VARIABLE='3-HPMA Urinary
Concentration Adjusted for Creatinine' || ' (' || left(strip(avalu)) ||
')'; /* 6) JMH 23Jun2014 */
        ELSE IF PARAMN=45 THEN VARIABLE='MHBMA Urinary
Concentration Adjusted for Creatinine' || ' (' || left(strip(avalu)) ||
')'; /* 6) JMH 23Jun2014 */
        ELSE IF PARAMN=66 THEN VARIABLE='S-PMA Urinary
Concentration Adjusted for Creatinine' || ' (' || left(strip(avalu)) ||
')'; /* 6) JMH 23Jun2014 */
    end;
    ELSE IF TYPE='abs' THEN DELETE; /* 1) SM 15May2014 */
    /*else if type='pch' then do; 1) SM 15May2014
        if paramn=2 then variable='%Change from Baseline in Evening COHb
(%)';
        else variable='%Change from Baseline in
'||trim(scan(param,1,'(')) || ' (%)';
    end; */

    if varname='N' then do;
        statord=1;
        stat='n';
    end;

        else if varname='BLQ' then do;
            statord=2;
            stat='BLOQ - n (%)';
            end;
        else if varname='GMEANCV' then do;
            statord=8;
            stat='GMean (CV%)';
            end;
    else if varname='CI' then do;
        statord=4;
        stat='95% CI';
    end;
    else if varname='MEDIAN' then do;
        statord=5;
        stat='Median';
    end;
    else if varname='QUART' then do;
        statord=6;
        stat='Q25, Q75';
    end;
    else if varname='MINMAX' then do;
        statord=7;
        stat='Min, Max';
    end;
    else if varname='MEANSD' then do;
        statord=3;
        stat='Mean (SD)';
    end;
    drop varname;
run;

data results07;

```

```

set results06;

if stat='N' then do;
    if missing(_1) then _1='0';
    if missing(_2) then _2='0';
    if missing(_3) then _3='0';
end;

/* 3) start JMH 11Jun2014 */
    ATTRIB BLQVAL LENGTH=$50.;
    IF PARAMN=45/*44*/ THEN BLQVAL='0.100 ng/mL'; /* 6) JMH
23Jun2014 */
    IF PARAMN=19/*50*/ THEN BLQVAL='20.0 ng/mL'; /* 6) JMH
23Jun2014 */
    IF PARAMN=66/*63*/ THEN BLQVAL='0.0250 ng/mL'; /* 6) JMH
23Jun2014 */
/* 3) end JMH 11Jun2014 */

/* 4) start JMH 19Jun2014 */ /* 6) JMH 23Jun2014 */
/*      IF PARAMN=44 THEN VARIABLE='MHBMA Urinary Concentration
Adjusted for Creatinine (ng/mg creat)';*/
/*      ELSE IF PARAMN=50 THEN VARIABLE='3-HPMA Urinary Concentration
Adjusted for Creatinine (ng/mg creat)';*/
/*      ELSE IF PARAMN=63 THEN VARIABLE='S-PMA Urinary Concentration
Adjusted for Creatinine (ng/mg creat)';*/
/* 4) end JMH 19Jun2014 */

/*IF PARAMN=2 AND STATORD=2 THEN DELETE;*/ /* 9) JMH
05Aug2014 */ /* 12) JMH 02Oct2014 */
run;

data labels;
set results07;
    attrib _1 label = "THS 2.2$(N=&trt1)"
           _2 label = "CC$(N=&trt2)"
           _3 label = "SA$(N=&trt3)";

                                flag=1;

run;

proc sql noprint;
    create table table.T_15_02_03_05 as
    select paramn, variable, type, statord, stat, _1, _2, _3
    from labels
    order by paramn, type, statord;
quit;

proc sort data=labels;
    by paramn type statord;
run;

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```

data paging;
  set labels;
  by paramn type statord;
  if first.type then ln=1; /*Amend to look presentable, and avoid page
overflows*/
  else ln+1;
  if ln=1 then page+1;
  call symput("page",compress(put(page,best.)));
run;

options number nodate orientation=landscape papersize=&p_pgsz missing='
';
ods escapechar='$';
%let linetop = \brdrt\brdrs\brdrw30; * needs to be 1.5pt so calculated
in twips (1/20 pt) ;
%let linebot = \brdrb\brdrs\brdrw30;

ods path stdlib.tl06324 (read) ;
ods results off;
ods rtf toc_data
file="/cvn/projects/prj/data/000000106324/TFL/&TFL_Part./&tflno..rtf"
style=tl06324 startpage=yes headery=1440 footery=1440 ;
ods noproctitle;

%do i=1 %to &page;

title ;
footnote;
%let wd=0;
%LET blq=0; /* 3) JMH 11Jun2014 */

data comp;
  set paging end=eof;
  where page=&i;
  CALL SYMPUT("blqval",LEFT(STRIP(BLQVAL))); /* 3) JMH 11Jun2014 */
  IF MISSING(BLQVAL) THEN CALL SYMPUT('blq',1); /* 3) JMH 11Jun2014
*/

  /* Amend title as needed */
  _firtitl="Table 15.2.3.5 Descriptive Statistics of % Change from
Baseline in Primary Biomarkers on Day 5 - FAS";
  _upcas=(length("Path: &TFLpath.")-
length(compress("Path:&TFLpath.",'ABCDEFGHIJKLMNOPQRSTUVWXYZ')))/2;
  len=&blankn.-length("(page &i of &page)");
  if eof then do;
    call symput('_FSRTITL', trim(left(_firtitl)));
    call symput('_blankn', compress(put(len,best.)));
  end;

  drop _firtitl _upcas len;
run;

```

```

ods proclabel = ' ';
ods listing close;

* most set up in template others below;
* title arial 12pt bold with 12pt paragraph space below;
* all headers to be arial 11pt bold;
* data arial 10pt;
* headers to be central, text values left aligned and numeric centered
around decimal point;
proc report data = comp missing headline headskip missing nowd split =
'$' %if &i=1 %then %do; contents=' ' %end; %else %do; contents='' %end;;;
    column flag page paramn type variable statord stat _1 _2 _3;

    define flag          / order order = internal noprint;
    define page          / order order = internal noprint;
    define paramn        / order order=internal noprint;
    define type          / order order=internal noprint;
    define variable      / group style={just=left cellwidth=3.9cm}
style(header)={just=center} "Variable"; /* 7) JMH 24Jun2014 */
    define statord       / order order = internal noprint;
    define stat          / display style={just=left cellwidth=1.5cm}
style(header)={just=center} "Statistic"; /* 7) JMH 24Jun2014 */
    define _1            / display style={just=CENTER/*d*/
cellwidth=1.4cm} style(header)={just=center}; /* 7) JMH 24Jun2014 */
    define _2            / display style={just=CENTER/*d*/
cellwidth=1.4cm} style(header)={just=center}; /* 7) JMH 24Jun2014 */
    define _3            / display style={just=CENTER/*d*/
cellwidth=1.4cm} style(header)={just=center}; /* 7) JMH 24Jun2014 */

    break before flag / page %if &i=1 %then %do;
    contents="&_fsrtitl" %end; %else %do; contents='' %end;;

    break after page / page;

    compute after variable;
        line " ";
    endcomp;

    compute before page / style={protectspecialchars=off};;
        line "&linetop";
    endcomp;

/*      compute after page/style={just=left cellwidth=5cm
protectspecialchars=off};*/ /* 8) JMH 01Aug2014 */
/*      line "&linebot" ;*/
/*      endcomp;*/

    compute before _page_ / style={just=left protectspecialchars=off};
        line "\b\fs24\sa24&_FSRTITL." ; * \b = bold, \fs24 is font
size 12pt, \sa24 is space after 12pt;
        line "&linebot";
    endcomp;

```

```

        compute after _page_/ style={just=left protectspecialchars=off
PRETEXT="&LINETOP."}; /* 8) JMH 01Aug2014 */
/*
        line 'Note: Arithmetic mean, SD and 95% confidence interval
(CI) of the mean are reported.';*/ /* 7) JMH 24Jun2014 */
        line 'Note: CC = Conventional cigarettes; SA = Smoking
abstinence; THS = Tobacco Heating System.';
        line 'Note: Percentages are based on the number of subjects
indicated in the column header (N).'; /* 8) JMH 01Aug2014 */
        *line 'Note: Baseline is defined as the last assessment prior to
06:29 AM on Day 1.'; /* 8) JMH 01Aug2014 */
line "Note: Baseline is the last assessment prior to first product use in
CC/THS 2.2 arms on Day 1 or last assessment prior to 06:29 AM in SA arm
on Day 1."; /* 10) JR 18Sep2014 */
        %if &nsum. ge 1 and &blq. ne 1 %then %do;
                /*line 'Note: LOQ = XX %';*/ /*Update this value if
required*/
                /*LINE "Note: LOQ = &blqval";          */ /* 3) JMH 11Jun2014 */
                /*LINE "Note: BLOQ = &blqval";*/ /* 5) JMH 19Jun2014 */
                LINE "Note: BLOQ = number of observations imputed using half
limit of quantification (&blqval)."; /* 8) JMH 01Aug2014 */
        %end;
        line ' ';
        line 'Appendix 15.3.3.1';
        line "Path: &TFLpath." &_blankn.*"\~\~" "(Page &i of &page)";
        line "Program Run: &sysdate  &sysuserid  Program Status:
&status";
        endcomp;
run;
%end;
ods rtf close;
ods results on;
ods path sashelp.tmplmst (read);

%mend ;

%outrtf(blankn=70, halfblnk=N);
ods listing;
proc printto print = "&table./T_15_02_03_05.lst" new;
run;

proc contents data = table.T_15_02_03_05 varnum;
run;
ods listing close;
proc printto ; run;
*=====;
* END OF PROGRAM CODE ;
*=====;

```