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*****;
* Project          : ZRHM-REXA-07-JP
*
* Program name     : T1502042501_ZRHM-REXA-07_V1.sas
*
* Author          : L. Yan
*
* Date created     : 05/20/2015
*
* Purpose         : Table T1502042501.
*
* Revision History :
*
* Date           Author      Ref      Revision (Date in YYYYMMDD format)
*
*****;

%let prgname=T1502042501_ZRHM_REXA_07_JP_V1;
options mprint;

options sasautos=("W:\pmp07\macros" sasautos) notes;
%*init(delivery=2);
%init(delivery=9);

%titlecsv(prgname=&prgname., version=5);

%put &title1;
%put &title2;
%put &APPENDIX;
%put &endpoint;
%put &outname.;
%put &repversion.;

options missing="";

%macro cal_summary_pvalue(wher=, outnum=, method=, used=, var=, in=, pflg=, paramcd=, avisit=);

title2 h=10pt j=1 "&used";

proc sort data=&in. out=anadt_&outnum.;
by usubjid;
where &wher. ;
run;

proc sort data=anadt_&outnum.;
by trtcd;
run;

%if &method = 1 %then %do;
title3 h=10pt j=1 "Paramcd: &paramcd, &avisit. Model: GLM, Method: Log";
proc means data = anadt_&outnum. noprint;
by trtcd;
var &var.;
output out=xlab_&outnum. n=n mean=mean median=med std=sd min=min max=max q1=q1 q3=q3 lclm=lclm uclm=uclm;
run;
%end;

%if &method = 2 %then %do;
title3 h=10pt j=1 "Paramcd: &paramcd, &avisit. Model: GLM, Method: Normal";

proc means data = anadt_&outnum. noprint;
by trtcd;
var aval;
output out=xlab_&outnum. n=n mean=mean median=med std=sd min=min max=max q1=q1 q3=q3 lclm=lclm uclm=uclm;
run;
%end;

data xlab_&outnum.;
set xlab_&outnum.;
n1 = trim(left(compress(put(n, 8.))));
if sd > . then mean1 = (trim(left(compress(put(mean, 8.1))))||' ('||trim(left(compress(put(ceil(sd*100)/100, 8.2))))||')');
else mean1 = (trim(left(compress(put(mean, 8.1))))||' (NA)');
ci1=trim(left(compress(put(floor(lclm*100)/100, 8.2))))||' , '||trim(left(compress(put(ceil(uclm*100)/100, 8.2)))));
median1 = trim(left(compress(put(med, 8.1))));
q1q3 = trim(left(compress(put(q1, 8.2))))||' , '||trim(left(compress(put(q3, 8.2))));
min1 = trim(left(compress(put(min, 8.))))||' , '||trim(left(compress(put(max, 8.0))));
run;

/*
proc mixed data=anadt_&outnum.;

Class trtcd sex UCPDGR1;

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Model logaval = logbase sex UCPDGR1 trtcd / outp=pred;

lsmeans trtcd / pdiff =control('mCC') alpha=0.05 cl;

ods output lsmeans=lsmeans_&outnum. (keep=trtcd lower upper estimate); *each arm;

ods output diffs=LSMeanDiffCL&outnum. (keep=trtcd lower upper probt estimate); * lsmean and C.I. for ratios;

ods output covparms=ROOTMSE&outnum.(rename=(estimate=mse)); *MSE;

run;
*/

proc glm data=anadt_&outnum.;
class trtp sex UCPDGR1;
%if &method = 1 %then %do;
model logaval = logbase sex UCPDGR1 trtp;
%end;
%if &method = 2 %then %do;
model aval = base sex UCPDGR1 trtp;
%end;
lsmeans trtp / pdiff =control('mCC') alpha=0.05 cl adjust=t;
lsmeans trtp / pdiff =control('SA') alpha=0.05 cl adjust=t;
ods output LSMeans=pval&outnum. (keep=ProbtDiff trtp where=(TRTP in ("THSm2.2"))); *p-value;
ods output LSMeanCL=lsmeans_&outnum. (keep=trtp lowercl uppercl lsmean); *lsmean, C.I. for each arm;
ods output LSMeanDiffCL=LSMeanDiffCL&outnum. (keep=trtp _trtp lowercl uppercl difference where=(TRTP in ("THSm2.2"))); *
lsmean and C.I. for ratios;
ods output FitStatistics=ROOTMSE&outnum. (keep=rootmse); *RootMSE;
run;quit;

ods output close;

data lsmeans_&outnum.;
set lsmeans_&outnum.;
if TRTP="THSm2.2" then trtcd=1;
else if TRTP="mCC" then trtcd=2;
else if TRTP="SA" then trtcd=3;

%if &method = 1 %then %do;
Estimate1 = exp(lsmean); /* Ratio of geometric mean */
LowerCL = exp(lowercl); /* 95% CI lower bound */
UpperCL = exp(uppercl); /* 95% CI upper bound */
%end;
%if &method = 2 %then %do;
Estimate1 = lsmean; /* Ratio of geometric mean */
LowerCL = lowercl; /* 95% CI lower bound */
UpperCL = uppercl; /* 95% CI upper bound */
%end;
run;

data ROOTMSE&outnum.;
set ROOTMSE&outnum.;
CVperc=100*sqrt(exp(rootmse**2)-1);
run;

proc sort data=lsmeans_&outnum. nodupkey;
by trtcd;
run;

data lsmeans_&outnum.;
length geomean geoci $100;
set lsmeans_&outnum.;
geomean=strip(put(ESTIMATE1, 8.2));
geoci=strip(put(floor(LowerCL*100)/100, 8.2)||", "||strip(put(ceil(UpperCL*100)/100, 8.2)));
keep trtcd geomean geoci;
run;

proc sort data=LSMeanDiffCL&outnum. nodup;
by TRTP _TRTP;
run;

data LSMeanDiffCL&outnum.;
set LSMeanDiffCL&outnum.;
myord=1;
run;

data ROOTMSE&outnum.;
set ROOTMSE&outnum.;
myord=1;
run;

data LSMeanDiffCL&outnum.;
merge LSMeanDiffCL&outnum. ROOTMSE&outnum.;
by myord;
run;

data LSMeanDiffCL&outnum.;

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length geomean geoci $100;
set LSMeanDiffCL&outnum.;
if _TRTP eq "mCC" then trtcd=4;
if _TRTP eq "SA" then trtcd=5;
%if &method = 1 %then %do;

    difference = 100*exp(difference); /* Ratio of geometric mean */
    lowercl = 100*exp(lowercl); /* 95% CI lower bound */
    uppercl = 100*exp(uppercl); /* 95% CI upper bound */
%end;

%if &method = 2 %then %do;

    difference =difference; /* Ratio of geometric mean */
    lowercl = lowercl; /* 95% CI lower bound */
    uppercl = uppercl; /* 95% CI upper bound */
%end;

%if &method = 1 %then %do;
geomean=strip(put(round(difference, 0.01), 8.2))||" ("||strip(put(ceil(CVperc*100)/100, 8.2)) ||")";
%end;
%if &method = 2 %then %do;
geomean=strip(put(round(difference, 0.01), 8.2))*"|" ("||strip(put(CVperc, 8.1)) ||")"/;
%end;

geoci=strip(put(floor(lowercl*100)/100, 8.2))||", "||strip(put(ceil(uppercl*100)/100, 8.2));
keep trtcd geomean geoci difference;
run;

data pval&outnum.;
set pval&outnum.;
if _n_=1;
trtcd=4;
keep trtcd ProbtDiff;
format ProbtDiff PVALUE6.3;
run;

proc sort data=LSMeanDiffCL&outnum.;
by trtcd;
run;

data LSMeanDiffCL&outnum.;
merge LSMeanDiffCL&outnum. pval&outnum.;
by trtcd;
run;

data LSMeanDiffCL&outnum.;
set LSMeanDiffCL&outnum.;
%if &method = 1 %then %do;
if (difference < 100) then ProbtDiff=ProbtDiff/2;
else ProbtDiff=1-ProbtDiff/2;
%end;
%if &method = 2 %then %do;
if (difference < 0) then ProbtDiff=ProbtDiff/2;
else ProbtDiff=1-ProbtDiff/2;
%end;
run;

data mrep_&outnum.;
set lsmeans_&outnum. LSMeanDiffCL&outnum.;
run;

proc sort data=mrep_&outnum.;
by trtcd;
run;

proc sort data=xlab_&outnum.;
by trtcd;
run;

data xlab_&outnum.;
merge xlab_&outnum. (in=a) mrep_&outnum.;
by trtcd;
run;

data xlab_&outnum.;
set xlab_&outnum.;
row0="";
if geoci ne "";
run;

proc transpose data = xlab_&outnum. out=xlab_1_&outnum.;
id trtcd;
var row0 n1 geomean geoci ProbtDiff;
run;

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data rep_&outnum.;
length _name_ _1 _2 _3 ord1 $100;
set xlab_1 &outnum.;
ord1="&outnum";
ordnum=input(ord1, best.);
if upcase(_name_)="ROW0" then do; _name_=" "; sord=-1; end;

if upcase(_name_)="N1" then do; _name_="n"; sord=0; end;
%if &method = 1 %then %do;
if upcase(_name_)="GEOMEAN" then do; _name_="Geometric LS Mean (CV%)"; sord=1; end;
if upcase(_name_)="GEOCI" then do; _name_="95% CI of Geometric Mean"; sord=2; end;
if upcase(_name_)="CI1" then do; _name_="95% CI of Mean"; sord=4; end;
%end;
%if &method = 2 %then %do;
if upcase(_name_)="GEOMEAN" then do; _name_="LS Mean"; sord=1; end;
if upcase(_name_)="GEOCI" then do; _name_="95% CI"; sord=2; end;
if upcase(_name_)="CI1" then do; _name_="95% CI"; sord=4; end;
%end;

if upcase(_name_)="MEAN1" then do; _name_="Mean (SD)"; sord=3; end;
if upcase(_name_)="MEDIAN1" then do; _name_="Median"; sord=5; end;
if upcase(_name_)="Q1Q3" then do; _name_="Q25, Q75"; sord=6; end;
if upcase(_name_)="MIN1" then do; _name_="Min, Max"; sord=7; end;
if upcase(_name_)="PROBTDIFF" then do; _name_="p-value (one-sided)"; sord=9; end;
run;

data rep;
set rep rep_&outnum.;
run;

%mend;

%macro mainloop(where1=, outn=, where=);

proc sort data=adam.adsl out=trt;
by usubjid;
where PPROT1FL="Y";
run;

data trt;
set trt;
if TRT01A="THSm2.2" then trtcd=1;
else if TRT01A="mCC" then trtcd=2;
else if TRT01A="SA" then trtcd=3;
run;

/*
"Use PPROTxxFL with xx in 1,2,3,4 for data at APUPER=1,2,3,4 respectively.

* Set A) ADAM.ADBX; PARAMCD in
- UTXB2CRE, UPGF2CRE (Day 5, Day 30, Day 60, Day 90)
* Set B.1) ADAM.ADLB; PARAMCD in
- ICAM1 (Day 6, Day 30, Day 60, Day 90)
* Set B.2)ADAM.ADLB; PARAMCD in
- HBA1C (Day 90)
- LDL, HDL, TRIG,CHOL (Day 30, Day 60, Day 90)
- WBC,NEUT,EOS,BASO,LYM,MONO (Day 6, Day 30, Day 60, Day 90)
* Set B.3)ADAM.ADLB; PARAMCD in
- CRP, FIBRINO, HOMOCY, GLUC (Day 30, Day 60, Day 90)
- PLAT (Day 6, Day 30, Day 60, Day 90)
* Set C) ADAM.ADVS; PARAMCD in
- SYSBP,DIABP (Day 6, Day 30, Day 60, Day 90)
- WEIGHT,WSTCIR (Day 90)
* Set D) ADAM.ADXP; PARAMCD=""FEVPCT""; PPROT4FL=""Y""; AVISIT=""DAY 91/DISCHARGE AMBULATORY""

*/

data indata1;
length group $4;
set adam.adbx;
group="A";
paramn=paramn+100;
if avisitn<=106 then used="The where clause used on the dataset adam.adbx: PPROT1FL=Y and ANL02FL=Y";
else if avisitn<=130 then used="The where clause used on the dataset adam.adbx: PPROT2FL=Y and ANL02FL=Y";
else if avisitn<=160 then used="The where clause used on the dataset adam.adbx: PPROT3FL=Y and ANL02FL=Y";
else if avisitn<=191 then used="The where clause used on the dataset adam.adbx: PPROT4FL=Y and ANL02FL=Y";

if PARAMCD in ("UTXB2CRE", "UPGF2CRE") and avisitn in (105, 130, 160, 190, 191) and ANL02FL="Y";
drop DTYPE ATPT;
run;

data indata2;
length group $4;
set adam.adlb;

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group="B1";
paramn=paramn+200;
if avisitn<=106 then used="The where clause used on the dataset adam.adlb: PPROT1FL=Y and ANL01FL=Y";
else if avisitn<=130 then used="The where clause used on the dataset adam.adlb: PPROT2FL=Y and ANL01FL=Y";
else if avisitn<=160 then used="The where clause used on the dataset adam.adlb: PPROT3FL=Y and ANL01FL=Y";
else if avisitn<=191 then used="The where clause used on the dataset adam.adlb: PPROT4FL=Y and ANL01FL=Y";

if paramcd in ("ICAM1") and avisitn in (106, 130, 160, 190, 191) and ANL01FL="Y";
drop DTYPE ATPT;
run;

data indata3;
length group $4;
set adam.adlb;
group="B2";
paramn=paramn+300;
if avisitn<=106 then used="The where clause used on the dataset adam.adlb: PPROT1FL=Y and ANL01FL=Y";
else if avisitn<=130 then used="The where clause used on the dataset adam.adlb: PPROT2FL=Y and ANL01FL=Y";
else if avisitn<=160 then used="The where clause used on the dataset adam.adlb: PPROT3FL=Y and ANL01FL=Y";
else if avisitn<=191 then used="The where clause used on the dataset adam.adlb: PPROT4FL=Y and ANL01FL=Y";

if (paramcd="HBA1C" and avisitn=190) or (paramcd in ("LDL", "HDL", "TRIG", "CHOL") and avisitn in (130, 160, 190, 191))
or (paramcd in ("WBC", "NEUT", "EOS", "BASO", "LYM", "MONO") and avisitn in (106, 130, 160, 190, 191)) and ANL01FL="Y";
drop DTYPE ATPT;
run;

data indata4;
length group $4;
set adam.adlb;
group="B3";
paramn=paramn+400;
if avisitn<=106 then used="The where clause used on the dataset adam.adlb: PPROT1FL=Y and ANL01FL=Y";
else if avisitn<=130 then used="The where clause used on the dataset adam.adlb: PPROT2FL=Y and ANL01FL=Y";
else if avisitn<=160 then used="The where clause used on the dataset adam.adlb: PPROT3FL=Y and ANL01FL=Y";
else if avisitn<=191 then used="The where clause used on the dataset adam.adlb: PPROT4FL=Y and ANL01FL=Y";
if (paramcd in ("CRP", "FIBRINO", "HOMOCY", "GLUC") and avisitn in (130, 160, 190, 191)) or (paramcd="PLAT" and avisitn
in (106, 130, 160, 190, 191)) and ANL01FL="Y";
drop DTYPE ATPT;
run;

data indata5;
length group $4;
set adam.advs;
group="C";
paramn=paramn+800;
if avisitn<=106 then used="The where clause used on the dataset adam.advs: PPROT1FL=Y and ANL01FL=Y";
else if avisitn<=130 then used="The where clause used on the dataset adam.advs: PPROT2FL=Y and ANL01FL=Y";
else if avisitn<=160 then used="The where clause used on the dataset adam.advs: PPROT3FL=Y and ANL01FL=Y";
else if avisitn<=191 then used="The where clause used on the dataset adam.advs: PPROT4FL=Y and ANL01FL=Y";

if (PARAMCD in ("SYSBP", "DIABP") and avisitn in (106, 130, 160, 190, 191)) or (paramcd in ("WEIGHT", "WSTCIR") and avis
itn=191) and ANL01FL="Y";
drop DTYPE ATPT;
run;
/*
data indata6;
length group $4;
set adam.adxp;
group="D";
paramn=paramn+500;
if avisitn<=106 then used="The where clause used on the dataset adam.adbx: PPROT1FL=Y and ANL01FL=Y";
else if avisitn<=130 then used="The where clause used on the dataset adam.adbx: PPROT2FL=Y and ANL01FL=Y";
else if avisitn<=160 then used="The where clause used on the dataset adam.adbx: PPROT3FL=Y and ANL01FL=Y";
else if avisitn<=191 then used="The where clause used on the dataset adam.adbx: PPROT4FL=Y and ANL01FL=Y";

if paramcd="FEVPCT" and avisitn=191 and ANL01FL="Y";
drop DTYPE ATPT;
run;
*/
/*
Blood pressure, HbA1c, LDL, HDL, TG, TC, WBC, BASO, EOS, MONO, NEUT, LYM, ,body weight and waist circumference will be a
nalyzed in the regular scale.
8-epi-PGF2a, 11 DTX-B2, sICAM will be analyzed in the logarithmic scale.
Other risk markers will be logarithmically transformed prior to analysis if there is evidence of non-normality by means
of Shapiro-Wilks test using baseline
data from FAS population - if p-val <= 0.05 then analyze in log scale; otherwise, use regular scale.
*/

data anlndata1;
set indata1-indata5;
if paramcd in ("SYSBP", "DIABP", "HBA1C", "LDL", "HDL", "TRIG", "CHOL", "WBC", "NEUT", "EOS", "BASO", "LYM", "MONO", "WEI
GHT", "WSTCIR", "FEVPCT") then method=2;
else if paramcd in ("UTXB2CRE", "UPGF2CRE", "ICAM1") then method=1;
else method=3;

if aval>0 then logaval=log(aval);
if base>0 then logbase=log(base);

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run;

proc sort data=anldata1 out=fmt(keep=paramn param) nodupkey;
by paramn param;
run;

proc sort data=anldata1 out=check(keep=method paramcd) nodupkey;
by method paramcd;
run;

data indata1 indata2;
set anldata1;
if method=3 then output indata2;
else output indata1;
run;

data indata2;
set indata2;
drop method;
run;

proc sort data=indata2;
by paramcd;
run;

proc sort data=test;
by paramcd;
run;

data indata2;
merge indata2 test;
by paramcd;
run;

data anldata1;
set indata1 indata2;
run;

data anldata1;
set anldata1;
if &where.;
run;

proc sort data=anldata1 out=check(keep=paramn avisitn avisit method used param paramcd) nodupkey;
by paramn avisitn avisit method;
where &where1.;
run;

data trt_1;
set trt;
run;

data anldata1;
set anldata1;
if TRTP="THSm2.2" then trtcd=1;
else if TRTP="mCC" then trtcd=2;
else if TRTP="SA" then trtcd=3;
run;

data check;
set check;
ord=_n_;
run;

%*cal_sumary_pvalue(where=1, outnum=1, var=aval, in=anldata1, pflg=1);

data rep;
run;

data _null_;
set check;
call execute ('%cal_sumary_pvalue(where=%str(avisitn=||avisitn|| and paramn=||paramn|| ), outnum=||ord||, method=||method||, used=||used||, var=logaval, in=anldata1, paramcd=||paramcd||, avisit=||avisit||);');
run;

data frep;
set rep;
ord=ORDNUM;
run;

data frep;
merge frep(in=a) check;
by ord;
if a;
if avisitn>.;
run;

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proc sort data=trt_1 nodupkey;
by trtcd usubjid;
run;

proc freq data = trt_1 noprint;
tables trtcd/ out= denom;
run;

data _null_;
set denom end=eof;

retain total 0;

total = total+count;

if trtcd= 1 then do;
call symput('trt1', trim(left(put(count,8)))));
end;
if trtcd= 2 then do;
call symput('trt2', trim(left(put(count,8)))));
end;
if trtcd= 3 then do;
call symput('trt3', trim(left(put(count,8)))));
end;
run;

%put trt1=&trt1 trt2=&trt2 trt3=&trt3;

%macro cal_part_main();

data frep;
set frep;

avisit=propcase(avisit);
if AVISIT="Day 0" then avisit="Baseline";

%do i = 1 %to 100;
if (&i-1)*3<ordnum<=&i*3 then pagen=&i;
%end;

run;

%mend;

%cal_part_main();
data frep&outn.;
set frep;
space="";
if _name_="p-value (one-sided)" then delete;
run;

%mend;

%trtrtfg(pgmname=&loutname., pgmid=1, new=0, style=, bookmark=%lowcase(&outname.));

title1 bold j=1 "&title1 &title2";
*footnote1 j=1 h=9pt "Study ID:ZRHM-REXA-07-JP Program: &fprgname..sas Status: &repversion./&fdate.";

title2 h=10pt j=1 "The where clause used on the dataset adam.adxp/adlb: FASFL=Y and avisitn=100";
title3 h=10pt j=1 "Shapiro-Wilk Test, Paramcd: CRP, FIBRINO, HOMOCY, GLUC, PLAT";

data base;
set adam.adxp (drop= ABLFL ATPT) adam.adlb(drop= ABLFL ATPT);
if paramcd in ("CRP", "FIBRINO", "HOMOCY", "GLUC", "PLAT") and avisitn =100 and fasfl="Y";
run;

proc sort data=base;
by paramcd;
run;

ods listing close;
ods output TestsForNormality=TestsForNormality;
proc univariate data=base normal;
by paramcd;
var aval;
run;
ods listing;
ods output close;

data test;

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set testsfornormality;
if TEST="Shapiro-Wilk";
run;

data test;
set test;
if PVALUE<=0.05 then method=1;
else method=2;
keep paramcd method;
run;

%mainloop(wherel=%str(method=1), outn=1, where=%str((avisitn<=106 and APUPER=1 and PPROT1FL="Y") or
(avisitn=130 and APUPER=2 and PPROT2FL="Y") or (avisitn=160 and APUPER=3 and PPROT3FL="Y") or (avisitn in (190, 191) /*a
nd APUPER=4*/ and PPROT4FL="Y") ));

%mainloop(wherel=%str(method=2), outn=2, where=%str((avisitn<=106 and APUPER=1 and PPROT1FL="Y") or
(avisitn=130 and APUPER=2 and PPROT2FL="Y") or (avisitn=160 and APUPER=3 and PPROT3FL="Y") or (avisitn in (190, 191) /*a
nd APUPER=4*/ and PPROT4FL="Y") ));

ods listing;
ods rtf close;

%*mainloop(flg=PPROT2FL, outn=2, where=%str(avisitn=130 and APUPER=2));
%*mainloop(flg=PPROT3FL, outn=3, where=%str(avisitn=160 and APUPER=3));
%*mainloop(flg=PPROT4FL, outn=4, where=%str(avisitn in (190, 191) and APUPER=4));

data odata.&prgname.;
set frep1 (in=a) frep2 (in=b) /*frep3 (in=c) frep4 (in=d)*/;
*if a then group="PPROT1FL";
*if b then group="PPROT2FL";
*if c then group="PPROT3FL";
*if d then group="PPROT4FL";
run;

/*
proc sort data=anldata1 out=fmt(keep=paramn param) nodupkey;
by paramn param;
run;
*/

data fmt;
set fmt;
fmtname="grp";
start=paramn;
label=param;
run;

proc format cntlin=fmt;
run;

%global totalpage1;

data _null_;
set frep1 end=eof;

if eof then do;
call symput('totalpage1', trim(left(put(pagen,8)))));
end;

run;

%put totalpage1=&totalpage1;

data frep2;
set frep2;
pagen=pagen+&totalpage1;
run;

%global totalpage2;
data _null_;
set frep2 end=eof;

if eof then do;
call symput('totalpage2', trim(left(put(pagen,8)))));
end;

run;

%put totalpage2=&totalpage2;

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%*title(prgname1=&prgname.);

%trtrtfg(pgmname=&outname., pgmid=1, new=0, style=, bookmark=%lowercase(&outname.));

/*****
title1 j=1 h=9pt "Study ID: ZRHM-REXA-07-JP" j=r "Page ^{thispage} of ^{lastpage}";
title2 " ";
title3 bold j=1 "&title1 &title2";

title5 "^R/RTF'\brdrb\brdrs ' ";

footnote1 "^R/RTF'\brdrb\brdrs ' ";
footnote2 j=1 h=9pt "Note: mCC = Menthol conventional cigarettes; SA = Smoking abstinence; THSm2.2 = Tobacco Heating Sys
tem 2.2 Menthol .";
footnote3 j=1 h=9pt "Note: Adjusted geometric least squares (LS) means and confidence intervals (CIs) from an ANCOVA mod
el conducted with baseline value, study arm, ";
footnote4 j=1 h=9pt "sex and mCC consumption reported at screening as fixed effect factors. ";
footnote5 j=1 h=9pt " ";
footnote6 j=1 h=9pt "Program: &fprgname." j=c "Status: Draft/&fdate." j=r "&APPENDIX.";
/*****/

%macro reppart;

%do i = 1 %to &totalpage1;

proc report data=frep1 headskip headline spacing=4 nowd split='-' style=[outputwidth=100%] style(header column)=[protec
tspecialchars=off];
column pagen paramn avisitn avisit sord _name_ _1 space _2 space _3 space _4 space _5;
where pagen=&i.;
define pagen /order order=internal noprint;
define paramn /order order=internal noprint;
define avisitn /order order=internal noprint;
define avisit /order "Variable" flow style(column)=[cellwidth=15% just=l];
define sord /order order=internal noprint;

define _name_ /display "Statistic" flow style(column)=[cellwidth=20% just=l];
define _1 /display "THSm2.2" flow style(column)=[cellwidth=10% just=c];
define space /display " " flow style(column)=[cellwidth=0.1% just=c];

define _2 /display "mCC" flow style(column)=[cellwidth=10% just=c];
define space /display " " flow style(column)=[cellwidth=0.1% just=c];

define _3 /display "SA" flow style(column)=[cellwidth=10% just=c];

define space /display " " flow style(column)=[cellwidth=0.1% just=c];

define _4 /display "THSm2.2 : mCC Ratio (%)" flow style(column)=[cellwidth=10% just=c];
define space /display " " flow style(column)=[cellwidth=0.1% just=c];

define _5 /display "THSm2.2 : SA Ratio (%)" flow style(column)=[cellwidth=10% just=c];

COMPUTE before paramn /style=[fontweight=bold];
LINE @1 paramn grp.;
ENDCOMP;

COMPUTE after avisitn ;
LINE @1 " ";
ENDCOMP;

break after pagen/page;

compute before pagen;
line @1 " ";
endcomp;

compute before _page_ /style=[fontweight=bold fontsize=3.75];
line @1 "&title1 &title2";
line @1 "^R/RTF'\brdrb\brdrs\brdrw30\brsp20\b ' ";
endcomp;

compute after _page_ /style=[fontsize=1.75];
line @1 "Note: mCC = Menthol conventional cigarettes; SA = Smoking abstinence; THSm2.2 = Tobacco Heating System 2.2 Ment
hol .";
line @1 "Note: Adjusted geometric least squares (LS) means and confidence intervals (CIs) from an ANCOVA model conducted
with baseline value, ";
line @1 "study arm, sex and mCC consumption reported at screening as fixed effect factors. ";
line @1 " ";
line @1 "&APPENDIX.";
line @1 "Study ID: ZRHM-REXA-07-JP Program: &fprgname..sas Status: &repversion./&fdate. Page: &i.
of &totalpage2";
endcomp;

```

```

run;
%end;

%do i = %eval(&&totalpage1+1) %to &totalpage2;

proc report data=frep2 headskip headline spacing=4 nowd split='-' style=[outputwidth=100%] style(header column)=[protec
tspecialchars=off];
where pagen=&i;
column pagen paramn avisitn avisit sord _name_ _1 space _2 space _3 space _4 space _5;
define pagen /order order=internal noprint;
define paramn /order order=internal noprint;
define avisitn /order order=internal noprint;
define avisit /order "Variable" flow style(column)=[cellwidth=15% just=l];
define sord /order order=internal noprint;

define _name_ /display "Statistic" flow style(column)=[cellwidth=10% just=l];
define _1 /display "THSm2.2" flow style(column)=[cellwidth=10% just=c];
define space /display " " flow style(column)=[cellwidth=0.1% just=c];

define _2 /display "mCC" flow style(column)=[cellwidth=10% just=c];
define space /display " " flow style(column)=[cellwidth=0.1% just=c];

define _3 /display "SA" flow style(column)=[cellwidth=10% just=c];

define space /display " " flow style(column)=[cellwidth=0.1% just=c];

define _4 /display "THSm2.2 - mCC" flow style(column)=[cellwidth=10% just=c];
define space /display " " flow style(column)=[cellwidth=0.1% just=c];

define _5 /display "THSm2.2 - SA" flow style(column)=[cellwidth=10% just=c];

COMPUTE before paramn /style=[fontweight=bold];
LINE @1 paramn grp.;
ENDCOMP;

COMPUTE after avisitn ;
LINE @1 "";
ENDCOMP;

break after pagen/page;
compute before pagen;
line @1 "";
endcomp;

compute before _page_ /style=[fontweight=bold fontsize=3.75];
line @1 "&title1 &title2";
line @1 "^R/RTF'\brdrb\brdrs\brdrw30\brsp20\b ' ' ";
endcomp;

compute after _page_ /style=[fontsize=1.75];
line @1 "Note: mCC = Menthol conventional cigarettes; SA = Smoking abstinence; THSm2.2 = Tobacco Heating System 2.2 Ment
hol.";
line @1 "Note: Adjusted geometric least squares (LS) means and confidence intervals (CIs) from an ANCOVA model conducted
with baseline value,";
line @1 "study arm, sex and mCC consumption reported at screening as fixed effect factors. ";
line @1 " ";
line @1 "&APPENDIX.";
line @1 "Study ID:ZRHM-REXA-07-JP Program: &fprgname..sas Status: &repversion./&fdate. Page: &i.
of &totalpage2";
endcomp;

run;
%end;

%mend;
%reppart;

ods listing;
ods rtf close;

```

