**S23 Fig.** The STATA code used for the Meta-analysis.

\*\*\*\*Primary analyses\*\*\*\*

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*IPD meta-analysis\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

use "G:\SMART BP IPD\Pooled analysis\BPSMART dataset\_Full.dta", clear

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*Systolic blood pressure\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

\*\*\*\*\*IPD mean change in sBP by study and level of intevention, adjusted by age, sex and baseline BP; \*\*\*\*\*\*\*\*\*\*\*\*

\*6 months

\*\*Control patients for HINTS complete (for individual study point estimates)

set more off

ipdmetan, study(Study) by(level\_of\_intervention) effect(Mean sBP diff) re lcols((count) Total\_population\_6m (sum) Control\_6m Intervention\_6m) ///

forest(graphregion(color(white)) graphregion(margin(zero)) favours(Favours intervention # Favours control) texts(105) astext(60) xlabel(-15(5)10) range(-15,10) ///

noadjust ysize(6) xsize(5.5)) : regress Change\_in\_sBP\_6m Allocation Age Sex CSBP\_Baseline Diabetes if Dataset\_ID==1 | Dataset\_ID==2 ///

| Dataset\_ID==4 | Dataset\_ID==5 | Dataset\_ID==7 | Dataset\_ID==8 | Dataset\_ID==9 | Dataset\_ID==10 | Dataset\_ID==11 ///

| Dataset\_ID==15 | Dataset\_ID==16 | Dataset\_ID==17 | Dataset\_ID==3 | Dataset\_ID==18 | Dataset\_ID==191 | Dataset\_ID==192 ///

| Dataset\_ID==131 | Dataset\_ID==132 | Dataset\_ID==133 | Dataset\_ID==20 | Dataset\_ID==121 | Dataset\_ID==122 | Dataset\_ID==22 | Dataset\_ID==23 | Dataset\_ID==25

\*\*Control patients for HINTS halved (for level 4 sub-group point estimate)

use "G:\SMART BP IPD\Pooled analysis\BPSMART dataset\_Full\_split2.dta", clear

set more off

ipdmetan, study(Study) by(level\_of\_intervention) effect(Mean sBP diff) re lcols((count) Total\_population\_6m (sum) Control\_6m Intervention\_6m) ///

forest(graphregion(color(white)) graphregion(margin(zero)) favours(Favours intervention # Favours control) texts(105) astext(60) xlabel(-15(5)10) range(-15,10) ///

noadjust ysize(6) xsize(5.5)) : regress Change\_in\_sBP\_6m Allocation Age Sex CSBP\_Baseline Diabetes if Dataset\_ID==1 | Dataset\_ID==2 ///

| Dataset\_ID==4 | Dataset\_ID==5 | Dataset\_ID==7 | Dataset\_ID==8 | Dataset\_ID==9 | Dataset\_ID==10 | Dataset\_ID==11 ///

| Dataset\_ID==15 | Dataset\_ID==16 | Dataset\_ID==17 | Dataset\_ID==3 | Dataset\_ID==18 | Dataset\_ID==191 | Dataset\_ID==192 ///

| Dataset\_ID==131 | Dataset\_ID==132 | Dataset\_ID==133 | Dataset\_ID==20 | Dataset\_ID==121 | Dataset\_ID==122 | Dataset\_ID==22 | Dataset\_ID==23 | Dataset\_ID==25

\*\*Control patients for HINTS, TYBC and wakefield split (for summary point estimate)

use "G:\SMART BP IPD\Pooled analysis\BPSMART dataset\_Full\_split.dta", clear

set more off

ipdmetan, study(Study) by(level\_of\_intervention) effect(Mean sBP diff) re lcols((count) Total\_population\_6m (sum) Control\_6m Intervention\_6m) ///

forest(graphregion(color(white)) graphregion(margin(zero)) favours(Favours intervention # Favours control) texts(105) astext(60) xlabel(-15(5)10) range(-15,10) ///

noadjust ysize(6) xsize(5.5)) : regress Change\_in\_sBP\_6m Allocation Age Sex CSBP\_Baseline Diabetes if Dataset\_ID==1 | Dataset\_ID==2 ///

| Dataset\_ID==4 | Dataset\_ID==5 | Dataset\_ID==7 | Dataset\_ID==8 | Dataset\_ID==9 | Dataset\_ID==10 | Dataset\_ID==11 ///

| Dataset\_ID==15 | Dataset\_ID==16 | Dataset\_ID==17 | Dataset\_ID==3 | Dataset\_ID==18 | Dataset\_ID==191 | Dataset\_ID==192 ///

| Dataset\_ID==131 | Dataset\_ID==132 | Dataset\_ID==133 | Dataset\_ID==20 | Dataset\_ID==121 | Dataset\_ID==122 | Dataset\_ID==22 | Dataset\_ID==23 | Dataset\_ID==25

\*12 months

\*\*Control patients for HINTS complete (for individual study point estimates)

use "G:\SMART BP IPD\Pooled analysis\BPSMART dataset\_Full.dta", clear

set more off

ipdmetan, study(Study) by(level\_of\_intervention) effect(Mean sBP diff) re lcols((count) Total\_population\_12m (sum) Control\_12m Intervention\_12m) ///

forest(graphregion(color(white)) graphregion(margin(zero)) favours(Favours intervention # Favours control) texts(105) astext(60) xlabel(-15(5)10) range(-15,10) ///

noadjust ysize(6) xsize(5.5)) : regress Change\_in\_sBP\_12m Allocation Age Sex CSBP\_Baseline Diabetes if Dataset\_ID==1 | Dataset\_ID==2 | Dataset\_ID==3 ///

| Dataset\_ID==6 | Dataset\_ID==5 | Dataset\_ID==7| Dataset\_ID==9 | Dataset\_ID==10 | Dataset\_ID==16 | Dataset\_ID==141 | Dataset\_ID==142 ///

| Dataset\_ID==191 | Dataset\_ID==192 | Dataset\_ID==131 | Dataset\_ID==132 | Dataset\_ID==133 | Dataset\_ID==20 | Dataset\_ID==121 | Dataset\_ID==122 | Dataset\_ID==24

\*\*Control patients for HINTS halved (for level 4 sub-group point estimate)

use "G:\SMART BP IPD\Pooled analysis\BPSMART dataset\_Full\_split2.dta", clear

set more off

ipdmetan, study(Study) by(level\_of\_intervention) effect(Mean sBP diff) re lcols((count) Total\_population\_12m (sum) Control\_12m Intervention\_12m) ///

forest(graphregion(color(white)) graphregion(margin(zero)) favours(Favours intervention # Favours control) texts(105) astext(60) xlabel(-15(5)10) range(-15,10) ///

noadjust ysize(6) xsize(5.5)) : regress Change\_in\_sBP\_12m Allocation Age Sex CSBP\_Baseline Diabetes if Dataset\_ID==1 | Dataset\_ID==2 | Dataset\_ID==3 ///

| Dataset\_ID==6 | Dataset\_ID==5 | Dataset\_ID==7| Dataset\_ID==9 | Dataset\_ID==10 | Dataset\_ID==16 | Dataset\_ID==141 | Dataset\_ID==142 ///

| Dataset\_ID==191 | Dataset\_ID==192 | Dataset\_ID==131 | Dataset\_ID==132 | Dataset\_ID==133 | Dataset\_ID==20 | Dataset\_ID==121 | Dataset\_ID==122 | Dataset\_ID==24

\*\*Control patients for HINTS, TYBC and wakefield split (for summary point estimate)

use "G:\SMART BP IPD\Pooled analysis\BPSMART dataset\_Full\_split.dta", clear

set more off

ipdmetan, study(Study) by(level\_of\_intervention) effect(Mean sBP diff) re lcols((count) Total\_population\_12m (sum) Control\_12m Intervention\_12m) ///

forest(graphregion(color(white)) graphregion(margin(zero)) favours(Favours intervention # Favours control) texts(105) astext(60) xlabel(-15(5)10) range(-15,10) ///

noadjust ysize(6) xsize(5.5)) : regress Change\_in\_sBP\_12m Allocation Age Sex CSBP\_Baseline Diabetes if Dataset\_ID==1 | Dataset\_ID==2 | Dataset\_ID==3 ///

| Dataset\_ID==6 | Dataset\_ID==5 | Dataset\_ID==7| Dataset\_ID==9 | Dataset\_ID==10 | Dataset\_ID==16 | Dataset\_ID==141 | Dataset\_ID==142 ///

| Dataset\_ID==191 | Dataset\_ID==192 | Dataset\_ID==131 | Dataset\_ID==132 | Dataset\_ID==133 | Dataset\_ID==20 | Dataset\_ID==121 | Dataset\_ID==122 | Dataset\_ID==24

\*18 months

\*\*Control patients for HINTS complete (for individual study point estimates)

use "G:\SMART BP IPD\Pooled analysis\BPSMART dataset\_Full.dta", clear

set more off

ipdmetan, study(Study) by(level\_of\_intervention) effect(Mean sBP diff) re lcols((count) Total\_population\_18m (sum) Control\_18m Intervention\_18m) ///

forest(graphregion(color(white)) graphregion(margin(zero)) favours(Favours intervention # Favours control) texts(105) astext(60) xlabel(-15(5)10) range(-15,10) ///

noadjust ysize(6) xsize(5.5)) : regress Change\_in\_sBP\_18m Allocation Age Sex CSBP\_Baseline Diabetes if Dataset\_ID==9 | Dataset\_ID==16 ///

| Dataset\_ID==131 | Dataset\_ID==132 | Dataset\_ID==133 | Dataset\_ID==121 | Dataset\_ID==122 | Dataset\_ID==211 | Dataset\_ID==212

\*\*Control patients for HINTS halved (for level 4 sub-group point estimate)

use "G:\SMART BP IPD\Pooled analysis\BPSMART dataset\_Full\_split2.dta", clear

set more off

ipdmetan, study(Study) by(level\_of\_intervention) effect(Mean sBP diff) re lcols((count) Total\_population\_18m (sum) Control\_18m Intervention\_18m) ///

forest(graphregion(color(white)) graphregion(margin(zero)) favours(Favours intervention # Favours control) texts(105) astext(60) xlabel(-15(5)10) range(-15,10) ///

noadjust ysize(6) xsize(5.5)) : regress Change\_in\_sBP\_18m Allocation Age Sex CSBP\_Baseline Diabetes if Dataset\_ID==9 | Dataset\_ID==16 ///

| Dataset\_ID==131 | Dataset\_ID==132 | Dataset\_ID==133 | Dataset\_ID==121 | Dataset\_ID==122 | Dataset\_ID==211 | Dataset\_ID==212

\*\*Control patients for HINTS, TYBC and wakefield split (for summary point estimate)

use "G:\SMART BP IPD\Pooled analysis\BPSMART dataset\_Full\_split.dta", clear

set more off

ipdmetan, study(Study) by(level\_of\_intervention) effect(Mean sBP diff) re lcols((count) Total\_population\_18m (sum) Control\_18m Intervention\_18m) ///

forest(graphregion(color(white)) graphregion(margin(zero)) favours(Favours intervention # Favours control) texts(105) astext(60) xlabel(-15(5)10) range(-15,10) ///

noadjust ysize(6) xsize(5.5)) : regress Change\_in\_sBP\_18m Allocation Age Sex CSBP\_Baseline Diabetes if Dataset\_ID==9 | Dataset\_ID==16 ///

| Dataset\_ID==131 | Dataset\_ID==132 | Dataset\_ID==133 | Dataset\_ID==121 | Dataset\_ID==122 | Dataset\_ID==211 | Dataset\_ID==212

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*Diastolic Blood pressure\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

\*\*\*\*\*IPD mean change in dBP by study and level of intevention, adjusted by age, sex and baseline BP; \*\*\*\*\*\*\*\*\*\*\*\*

\*6 months

\*\*Control patients for HINTS complete (for individual study point estimates)

set more off

ipdmetan, study(Study) by(level\_of\_intervention) effect(Mean dBP diff) re lcols((count) Total\_population\_6m (sum) Control\_6m Intervention\_6m) ///

forest(graphregion(color(white)) graphregion(margin(zero)) favours(Favours intervention # Favours control) texts(105) astext(60) xlabel(-10(5)5) range(-10,5) ///

noadjust ysize(6) xsize(5.5)) : regress Change\_in\_dBP\_6m Allocation Age Sex CDBP\_Baseline Diabetes if Dataset\_ID==1 | Dataset\_ID==2 ///

| Dataset\_ID==4 | Dataset\_ID==5 | Dataset\_ID==7 | Dataset\_ID==8 | Dataset\_ID==9 | Dataset\_ID==10 | Dataset\_ID==11 ///

| Dataset\_ID==15 | Dataset\_ID==16 | Dataset\_ID==17 | Dataset\_ID==3 | Dataset\_ID==18 | Dataset\_ID==191 | Dataset\_ID==192 ///

| Dataset\_ID==131 | Dataset\_ID==132 | Dataset\_ID==133 | Dataset\_ID==20 | Dataset\_ID==121 | Dataset\_ID==122 | Dataset\_ID==22 | Dataset\_ID==23 | Dataset\_ID==25

\*\*Control patients for HINTS halved (for level 4 sub-group point estimate)

use "G:\SMART BP IPD\Pooled analysis\BPSMART dataset\_Full\_split2.dta", clear

set more off

ipdmetan, study(Study) by(level\_of\_intervention) effect(Mean dBP diff) re lcols((count) Total\_population\_6m (sum) Control\_6m Intervention\_6m) ///

forest(graphregion(color(white)) graphregion(margin(zero)) favours(Favours intervention # Favours control) texts(105) astext(60) xlabel(-10(5)5) range(-10,5) ///

noadjust ysize(6) xsize(5.5)) : regress Change\_in\_dBP\_6m Allocation Age Sex CDBP\_Baseline Diabetes if Dataset\_ID==1 | Dataset\_ID==2 ///

| Dataset\_ID==4 | Dataset\_ID==5 | Dataset\_ID==7 | Dataset\_ID==8 | Dataset\_ID==9 | Dataset\_ID==10 | Dataset\_ID==11 ///

| Dataset\_ID==15 | Dataset\_ID==16 | Dataset\_ID==17 | Dataset\_ID==3 | Dataset\_ID==18 | Dataset\_ID==191 | Dataset\_ID==192 ///

| Dataset\_ID==131 | Dataset\_ID==132 | Dataset\_ID==133 | Dataset\_ID==20 | Dataset\_ID==121 | Dataset\_ID==122 | Dataset\_ID==22 | Dataset\_ID==23 | Dataset\_ID==25

\*\*Control patients for HINTS, TYBC and wakefield split (for summary point estimate)

use "G:\SMART BP IPD\Pooled analysis\BPSMART dataset\_Full\_split.dta", clear

set more off

ipdmetan, study(Study) by(level\_of\_intervention) effect(Mean dBP diff) re lcols((count) Total\_population\_6m (sum) Control\_6m Intervention\_6m) ///

forest(graphregion(color(white)) graphregion(margin(zero)) favours(Favours intervention # Favours control) texts(105) astext(60) xlabel(-10(5)5) range(-10,5) ///

noadjust ysize(6) xsize(5.5)) : regress Change\_in\_dBP\_6m Allocation Age Sex CDBP\_Baseline Diabetes if Dataset\_ID==1 | Dataset\_ID==2 ///

| Dataset\_ID==4 | Dataset\_ID==5 | Dataset\_ID==7 | Dataset\_ID==8 | Dataset\_ID==9 | Dataset\_ID==10 | Dataset\_ID==11 ///

| Dataset\_ID==15 | Dataset\_ID==16 | Dataset\_ID==17 | Dataset\_ID==3 | Dataset\_ID==18 | Dataset\_ID==191 | Dataset\_ID==192 ///

| Dataset\_ID==131 | Dataset\_ID==132 | Dataset\_ID==133 | Dataset\_ID==20 | Dataset\_ID==121 | Dataset\_ID==122 | Dataset\_ID==22 | Dataset\_ID==23 | Dataset\_ID==25

\*12 months

\*\*Control patients for HINTS complete (for individual study point estimates)

use "G:\SMART BP IPD\Pooled analysis\BPSMART dataset\_Full.dta", clear

set more off

ipdmetan, study(Study) by(level\_of\_intervention) effect(Mean dBP diff) re lcols((count) Total\_population\_12m (sum) Control\_12m Intervention\_12m) ///

forest(graphregion(color(white)) graphregion(margin(zero)) favours(Favours intervention # Favours control) texts(105) astext(60) xlabel(-10(5)5) range(-10,5) ///

noadjust ysize(6) xsize(5.5)) : regress Change\_in\_dBP\_12m Allocation Age Sex CDBP\_Baseline Diabetes if Dataset\_ID==1 | Dataset\_ID==2 | Dataset\_ID==3 ///

| Dataset\_ID==6 | Dataset\_ID==5 | Dataset\_ID==7| Dataset\_ID==9 | Dataset\_ID==10 | Dataset\_ID==16 | Dataset\_ID==141 | Dataset\_ID==142 ///

| Dataset\_ID==191 | Dataset\_ID==192 | Dataset\_ID==131 | Dataset\_ID==132 | Dataset\_ID==133 | Dataset\_ID==20 | Dataset\_ID==121 | Dataset\_ID==122 | Dataset\_ID==24

\*\*Control patients for HINTS halved (for level 4 sub-group point estimate)

use "G:\SMART BP IPD\Pooled analysis\BPSMART dataset\_Full\_split2.dta", clear

set more off

ipdmetan, study(Study) by(level\_of\_intervention) effect(Mean dBP diff) re lcols((count) Total\_population\_12m (sum) Control\_12m Intervention\_12m) ///

forest(graphregion(color(white)) graphregion(margin(zero)) favours(Favours intervention # Favours control) texts(105) astext(60) xlabel(-10(5)5) range(-10,5) ///

noadjust ysize(6) xsize(5.5)) : regress Change\_in\_dBP\_12m Allocation Age Sex CDBP\_Baseline Diabetes if Dataset\_ID==1 | Dataset\_ID==2 | Dataset\_ID==3 ///

| Dataset\_ID==6 | Dataset\_ID==5 | Dataset\_ID==7| Dataset\_ID==9 | Dataset\_ID==10 | Dataset\_ID==16 | Dataset\_ID==141 | Dataset\_ID==142 ///

| Dataset\_ID==191 | Dataset\_ID==192 | Dataset\_ID==131 | Dataset\_ID==132 | Dataset\_ID==133 | Dataset\_ID==20 | Dataset\_ID==121 | Dataset\_ID==122 | Dataset\_ID==24

\*\*Control patients for HINTS, TYBC and wakefield split (for summary point estimate)

use "G:\SMART BP IPD\Pooled analysis\BPSMART dataset\_Full\_split.dta", clear

set more off

ipdmetan, study(Study) by(level\_of\_intervention) effect(Mean dBP diff) re lcols((count) Total\_population\_12m (sum) Control\_12m Intervention\_12m) ///

forest(graphregion(color(white)) graphregion(margin(zero)) favours(Favours intervention # Favours control) texts(105) astext(60) xlabel(-10(5)5) range(-10,5) ///

noadjust ysize(6) xsize(5.5)) : regress Change\_in\_dBP\_12m Allocation Age Sex CDBP\_Baseline Diabetes if Dataset\_ID==1 | Dataset\_ID==2 | Dataset\_ID==3 ///

| Dataset\_ID==6 | Dataset\_ID==5 | Dataset\_ID==7| Dataset\_ID==9 | Dataset\_ID==10 | Dataset\_ID==16 | Dataset\_ID==141 | Dataset\_ID==142 ///

| Dataset\_ID==191 | Dataset\_ID==192 | Dataset\_ID==131 | Dataset\_ID==132 | Dataset\_ID==133 | Dataset\_ID==20 | Dataset\_ID==121 | Dataset\_ID==122 | Dataset\_ID==24

\*18 months

\*\*Control patients for HINTS complete (for individual study point estimates)

use "G:\SMART BP IPD\Pooled analysis\BPSMART dataset\_Full.dta", clear

set more off

ipdmetan, study(Study) by(level\_of\_intervention) effect(Mean dBP diff) re lcols((count) Total\_population\_18m (sum) Control\_18m Intervention\_18m) ///

forest(graphregion(color(white)) graphregion(margin(zero)) favours(Favours intervention # Favours control) texts(105) astext(60) xlabel(-10(5)5) range(-10,5) ///

noadjust ysize(6) xsize(5.5)) : regress Change\_in\_dBP\_18m Allocation Age Sex CSBP\_Baseline Diabetes if Dataset\_ID==9 | Dataset\_ID==16 ///

| Dataset\_ID==131 | Dataset\_ID==132 | Dataset\_ID==133 | Dataset\_ID==121 | Dataset\_ID==122 | Dataset\_ID==211 | Dataset\_ID==212

\*\*Control patients for HINTS halved (for level 4 sub-group point estimate)

use "G:\SMART BP IPD\Pooled analysis\BPSMART dataset\_Full\_split2.dta", clear

set more off

ipdmetan, study(Study) by(level\_of\_intervention) effect(Mean dBP diff) re lcols((count) Total\_population\_18m (sum) Control\_18m Intervention\_18m) ///

forest(graphregion(color(white)) graphregion(margin(zero)) favours(Favours intervention # Favours control) texts(105) astext(60) xlabel(-10(5)5) range(-10,5) ///

noadjust ysize(6) xsize(5.5)) : regress Change\_in\_dBP\_18m Allocation Age Sex CSBP\_Baseline Diabetes if Dataset\_ID==9 | Dataset\_ID==16 ///

| Dataset\_ID==131 | Dataset\_ID==132 | Dataset\_ID==133 | Dataset\_ID==121 | Dataset\_ID==122 | Dataset\_ID==211 | Dataset\_ID==212

\*\*Control patients for HINTS, TYBC and wakefield split (for summary point estimate)

use "G:\SMART BP IPD\Pooled analysis\BPSMART dataset\_Full\_split.dta", clear

set more off

ipdmetan, study(Study) by(level\_of\_intervention) effect(Mean sBP diff) re lcols((count) Total\_population\_18m (sum) Control\_18m Intervention\_18m) ///

forest(graphregion(color(white)) graphregion(margin(zero)) favours(Favours intervention # Favours control) texts(105) astext(60) xlabel(-10(5)5) range(-10,5) ///

noadjust ysize(6) xsize(5.5)) : regress Change\_in\_dBP\_18m Allocation Age Sex CSBP\_Baseline Diabetes if Dataset\_ID==9 | Dataset\_ID==16 ///

| Dataset\_ID==131 | Dataset\_ID==132 | Dataset\_ID==133 | Dataset\_ID==121 | Dataset\_ID==122 | Dataset\_ID==211 | Dataset\_ID==212

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*Relative risk of blood pressure (systolic or diastolic) control\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

\*\*\*RR of BP control by study and level of intevention, adjusted by age, sex and baseline BP\*\*\*\*\*\*\*\*\*\*

\*6 months

\*\*Control patients for HINTS complete (for individual study point estimates)

use "G:\SMART BP IPD\Pooled analysis\BPSMART dataset\_Full.dta", clear

set more off

recode BP\_control\_6m (1=2)

recode BP\_control\_6m (0=1)

recode BP\_control\_6m (2=0)

ipdmetan, study(Study) by(level\_of\_intervention) effect(RR of BP control) lcols((count) Total\_population\_6m (sum) Control\_6m Intervention\_6m) ///

forest(graphregion(color(white)) graphregion(margin(zero)) favours(Favours intervention # Favours control) texts(100) astext(60) xlabel(0.5(1)2.5) range(0.1,2.5) ///

noadjust ysize(6.95) xsize(6)) rrr re: mlogit BP\_control\_6m Allocation Age Sex CSBP\_Baseline CDBP\_Baseline Diabetes ///

if Dataset\_ID==1 | Dataset\_ID==2 | Dataset\_ID==3 | Dataset\_ID==131 | Dataset\_ID==132 | Dataset\_ID==133 ///

| Dataset\_ID==4 | Dataset\_ID==5 | Dataset\_ID==7 | Dataset\_ID==8 | Dataset\_ID==9 | Dataset\_ID==10 | Dataset\_ID==11 ///

| Dataset\_ID==15 | Dataset\_ID==16 | Dataset\_ID==17 | Dataset\_ID==18 | Dataset\_ID==191 | Dataset\_ID==192 | Dataset\_ID==20 | Dataset\_ID==121 | Dataset\_ID==122 ///

| Dataset\_ID==22 | Dataset\_ID==23 | Dataset\_ID==25, baseoutcome(0)

\*\*Control patients for HINTS halved (for level 4 sub-group point estimate)

use "G:\SMART BP IPD\Pooled analysis\BPSMART dataset\_Full\_split2.dta", clear

set more off

recode BP\_control\_6m (1=2)

recode BP\_control\_6m (0=1)

recode BP\_control\_6m (2=0)

ipdmetan, study(Study) by(level\_of\_intervention) effect(RR of BP control) lcols((count) Total\_population\_6m (sum) Control\_6m Intervention\_6m) ///

forest(graphregion(color(white)) graphregion(margin(zero)) favours(Favours intervention # Favours control) texts(100) astext(60) xlabel(0.5(1)2.5) range(0.1,2.5) ///

noadjust ysize(6.95) xsize(6)) rrr re: mlogit BP\_control\_6m Allocation Age Sex CSBP\_Baseline CDBP\_Baseline Diabetes ///

if Dataset\_ID==1 | Dataset\_ID==2 | Dataset\_ID==3 | Dataset\_ID==131 | Dataset\_ID==132 | Dataset\_ID==133 ///

| Dataset\_ID==4 | Dataset\_ID==5 | Dataset\_ID==7 | Dataset\_ID==8 | Dataset\_ID==9 | Dataset\_ID==10 | Dataset\_ID==11 ///

| Dataset\_ID==15 | Dataset\_ID==16 | Dataset\_ID==17 | Dataset\_ID==18 | Dataset\_ID==191 | Dataset\_ID==192 | Dataset\_ID==20 | Dataset\_ID==121 | Dataset\_ID==122 ///

| Dataset\_ID==22 | Dataset\_ID==23 | Dataset\_ID==25, baseoutcome(0)

\*\*Control patients for HINTS, TYBC and wakefield split (for summary point estimate)

use "G:\SMART BP IPD\Pooled analysis\BPSMART dataset\_Full\_split.dta", clear

set more off

recode BP\_control\_6m (1=2)

recode BP\_control\_6m (0=1)

recode BP\_control\_6m (2=0)

ipdmetan, study(Study) by(level\_of\_intervention) effect(RR of BP control) lcols((count) Total\_population\_6m (sum) Control\_6m Intervention\_6m) ///

forest(graphregion(color(white)) graphregion(margin(zero)) favours(Favours intervention # Favours control) texts(100) astext(60) xlabel(0.5(1)2.5) range(0.1,2.5) ///

noadjust ysize(6.95) xsize(6)) rrr re: mlogit BP\_control\_6m Allocation Age Sex CSBP\_Baseline CDBP\_Baseline Diabetes ///

if Dataset\_ID==1 | Dataset\_ID==2 | Dataset\_ID==3 | Dataset\_ID==131 | Dataset\_ID==132 | Dataset\_ID==133 ///

| Dataset\_ID==4 | Dataset\_ID==5 | Dataset\_ID==7 | Dataset\_ID==8 | Dataset\_ID==9 | Dataset\_ID==10 | Dataset\_ID==11 ///

| Dataset\_ID==15 | Dataset\_ID==16 | Dataset\_ID==17 | Dataset\_ID==18 | Dataset\_ID==191 | Dataset\_ID==192 | Dataset\_ID==20 | Dataset\_ID==121 | Dataset\_ID==122

| Dataset\_ID==22 | Dataset\_ID==23 | Dataset\_ID==25, baseoutcome(0)

\*12 months

\*\*Control patients for HINTS complete (for individual study point estimates)

use "G:\SMART BP IPD\Pooled analysis\BPSMART dataset\_Full.dta", clear

set more off

recode BP\_control\_12m (1=2)

recode BP\_control\_12m (0=1)

recode BP\_control\_12m (2=0)

ipdmetan, study(Study) by(level\_of\_intervention) effect(RR of BP control) lcols((count) Total\_population\_12m (sum) Control\_12m Intervention\_12m) ///

forest(graphregion(color(white)) graphregion(margin(zero)) favours(Favours intervention # Favours control) texts(100) astext(60) xlabel(0.5(1)2.5) range(0.1,2.5) ///

noadjust ysize(6.95) xsize(6)) rrr re: mlogit BP\_control\_12m Allocation Age Sex CSBP\_Baseline CDBP\_Baseline Diabetes if Dataset\_ID==1 | Dataset\_ID==2 | Dataset\_ID==3 ///

| Dataset\_ID==6 | Dataset\_ID==5 | Dataset\_ID==7| Dataset\_ID==9 | Dataset\_ID==10 | Dataset\_ID==16 | Dataset\_ID==141 | Dataset\_ID==142 ///

| Dataset\_ID==191 | Dataset\_ID==192 | Dataset\_ID==131 | Dataset\_ID==132 | Dataset\_ID==133 | Dataset\_ID==20 | Dataset\_ID==121 | Dataset\_ID==122 | Dataset\_ID==24, baseoutcome(0)

\*\*Control patients for HINTS halved (for level 4 sub-group point estimate)

use "G:\SMART BP IPD\Pooled analysis\BPSMART dataset\_Full\_split2.dta", clear

set more off

recode BP\_control\_12m (1=2)

recode BP\_control\_12m (0=1)

recode BP\_control\_12m (2=0)

ipdmetan, study(Study) by(level\_of\_intervention) effect(RR of BP control) lcols((count) Total\_population\_12m (sum) Control\_12m Intervention\_12m) ///

forest(graphregion(color(white)) graphregion(margin(zero)) favours(Favours intervention # Favours control) texts(100) astext(60) xlabel(0.5(1)2.5) range(0.1,2.5) ///

noadjust ysize(6.95) xsize(6)) rrr re: mlogit BP\_control\_12m Allocation Age Sex CSBP\_Baseline CDBP\_Baseline Diabetes if Dataset\_ID==1 | Dataset\_ID==2 | Dataset\_ID==3 ///

| Dataset\_ID==6 | Dataset\_ID==5 | Dataset\_ID==7| Dataset\_ID==9 | Dataset\_ID==10 | Dataset\_ID==16 | Dataset\_ID==141 | Dataset\_ID==142 ///

| Dataset\_ID==191 | Dataset\_ID==192 | Dataset\_ID==131 | Dataset\_ID==132 | Dataset\_ID==133 | Dataset\_ID==20 | Dataset\_ID==121 | Dataset\_ID==122 | Dataset\_ID==24, baseoutcome(0)

\*\*Control patients for HINTS, TYBC and wakefield split (for summary point estimate)

use "G:\SMART BP IPD\Pooled analysis\BPSMART dataset\_Full\_split.dta", clear

set more off

recode BP\_control\_12m (1=2)

recode BP\_control\_12m (0=1)

recode BP\_control\_12m (2=0)

ipdmetan, study(Study) by(level\_of\_intervention) effect(RR of BP control) lcols((count) Total\_population\_12m (sum) Control\_12m Intervention\_12m) ///

forest(graphregion(color(white)) graphregion(margin(zero)) favours(Favours intervention # Favours control) texts(100) astext(60) xlabel(0.5(1)2.5) range(0.1,2.5) ///

noadjust ysize(6.95) xsize(6)) rrr re: mlogit BP\_control\_12m Allocation Age Sex CSBP\_Baseline CDBP\_Baseline Diabetes if Dataset\_ID==1 | Dataset\_ID==2 | Dataset\_ID==3 ///

| Dataset\_ID==6 | Dataset\_ID==5 | Dataset\_ID==7| Dataset\_ID==9 | Dataset\_ID==10 | Dataset\_ID==16 | Dataset\_ID==141 | Dataset\_ID==142 ///

| Dataset\_ID==191 | Dataset\_ID==192 | Dataset\_ID==131 | Dataset\_ID==132 | Dataset\_ID==133 | Dataset\_ID==20 | Dataset\_ID==121 | Dataset\_ID==122 | Dataset\_ID==24, baseoutcome(0)

\*18 months

\*\*Control patients for HINTS complete (for individual study point estimates)

use "G:\SMART BP IPD\Pooled analysis\BPSMART dataset\_Full.dta", clear

set more off

recode BP\_control\_18m (1=2)

recode BP\_control\_18m (0=1)

recode BP\_control\_18m (2=0)

ipdmetan, study(Study) by(level\_of\_intervention) effect(RR of BP control) lcols((count) Total\_population\_18m (sum) Control\_18m Intervention\_18m) ///

forest(graphregion(color(white)) graphregion(margin(zero)) favours(Favours intervention # Favours control) texts(100) astext(60) xlabel(0.5(1)2.5) range(0.1,2.5) ///

noadjust ysize(6.95) xsize(6)) rrr re: mlogit BP\_control\_18m Allocation Age Sex CSBP\_Baseline CDBP\_Baseline Diabetes if Dataset\_ID==9 | Dataset\_ID==16 ///

| Dataset\_ID==131 | Dataset\_ID==132 | Dataset\_ID==133 | Dataset\_ID==121 | Dataset\_ID==122 | Dataset\_ID==211 | Dataset\_ID==212, baseoutcome(0)

\*\*Control patients for HINTS halved (for level 4 sub-group point estimate)

use "G:\SMART BP IPD\Pooled analysis\BPSMART dataset\_Full\_split2.dta", clear

set more off

recode BP\_control\_18m (1=2)

recode BP\_control\_18m (0=1)

recode BP\_control\_18m (2=0)

ipdmetan, study(Study) by(level\_of\_intervention) effect(RR of BP control) lcols((count) Total\_population\_18m (sum) Control\_18m Intervention\_18m) ///

forest(graphregion(color(white)) graphregion(margin(zero)) favours(Favours intervention # Favours control) texts(100) astext(60) xlabel(0.5(1)2.5) range(0.1,2.5) ///

noadjust ysize(6.95) xsize(6)) rrr re: mlogit BP\_control\_18m Allocation Age Sex CSBP\_Baseline CDBP\_Baseline Diabetes if Dataset\_ID==9 | Dataset\_ID==16 ///

| Dataset\_ID==131 | Dataset\_ID==132 | Dataset\_ID==133 | Dataset\_ID==121 | Dataset\_ID==122 | Dataset\_ID==211 | Dataset\_ID==212, baseoutcome(0)

\*\*Control patients for HINTS, TYBC and wakefield split (for summary point estimate)

use "G:\SMART BP IPD\Pooled analysis\BPSMART dataset\_Full\_split.dta", clear

set more off

recode BP\_control\_18m (1=2)

recode BP\_control\_18m (0=1)

recode BP\_control\_18m (2=0)

ipdmetan, study(Study) by(level\_of\_intervention) effect(RR of BP control) lcols((count) Total\_population\_18m (sum) Control\_18m Intervention\_18m) ///

forest(graphregion(color(white)) graphregion(margin(zero)) favours(Favours intervention # Favours control) texts(100) astext(60) xlabel(0.5(1)2.5) range(0.1,2.5) ///

noadjust ysize(6.95) xsize(6)) rrr re: mlogit BP\_control\_18m Allocation Age Sex CSBP\_Baseline CDBP\_Baseline Diabetes if Dataset\_ID==9 | Dataset\_ID==16 ///

| Dataset\_ID==131 | Dataset\_ID==132 | Dataset\_ID==133 | Dataset\_ID==121 | Dataset\_ID==122 | Dataset\_ID==211 | Dataset\_ID==212, baseoutcome(0)

\*\*\*\*\*\*\*\*\*\*ABPM\*\*\*\*\*\*\*\*\*\*\*\*

\*\*\*\*Calculate change in Blood pressure at follow-up\*\*\*

gen Change\_in\_AsBPM\_6m = ABPM\_Daytime\_sys\_6months-ABPM\_Daytime\_sys\_baseline

gen Change\_in\_AdBPM\_6m = ABPM\_Daytime\_dia\_6months-ABPM\_Daytime\_dia\_baseline

gen Change\_in\_AsBPM\_12m = ABPM\_Daytime\_sys\_12months-ABPM\_Daytime\_sys\_baseline

gen Change\_in\_AdBPM\_12m = ABPM\_Daytime\_dia\_12months-ABPM\_Daytime\_dia\_baseline

\*\*\*\*\*IPD mean change in sBP at follow-up by study, adjusted by age, sex and baseline BP\*\*\*\*\*\*\*\*\*\*\*\*

\*Clinic 6 mths

set more off

ipdmetan, study(Study) effect(Mean sBP diff) re lcols((count) Total\_population\_6m (sum) Control\_6m Intervention\_6m) forest(graphregion(color(white)) ///

graphregion(margin(zero)) favours(Favours intervention # Favours control) texts(105) astext(60) xlabel(-10(5)5) range(-10,5.5) noadjust ysize(3) xsize(6)) ///

: regress Change\_in\_sBP\_6m Allocation Age Sex CSBP\_Baseline Diabetes level\_of\_intervention if Dataset==4|Dataset==5| Dataset==7 | Dataset==8 | Dataset==9

\*Ambulatory 6 mths

set more off

ipdmetan, study(Study) effect(Mean sBP diff) re lcols((count) Total\_population\_6m (sum) Control\_6m Intervention\_6m) forest(graphregion(color(white)) ///

graphregion(margin(zero)) favours(Favours intervention # Favours control) texts(105) astext(60) xlabel(-10(5)5) range(-10,5.5) noadjust ysize(3) xsize(6)) ///

: regress Change\_in\_AsBPM\_6m Allocation Age Sex CSBP\_Baseline Diabetes level\_of\_intervention if Dataset==4|Dataset==5| Dataset==7 | Dataset==8 | Dataset==9

\*Clinic 12 mths

set more off

ipdmetan, study(Study) effect(Mean sBP diff) re lcols((count) Total\_population\_12m (sum) Control\_12m Intervention\_12m) forest(graphregion(color(white)) ///

graphregion(margin(zero)) favours(Favours intervention # Favours control) texts(105) astext(60) xlabel(-10(5)5) range(-10,5.5) noadjust ysize(3) xsize(6)) ///

: regress Change\_in\_sBP\_12m Allocation Age Sex CSBP\_Baseline Diabetes level\_of\_intervention if Dataset==6|Dataset==5| Dataset==7 | Dataset==9

\*Ambulatory 12 mths

set more off

ipdmetan, study(Study) effect(Mean sBP diff) re lcols((count) Total\_population\_12m (sum) Control\_12m Intervention\_12m) forest(graphregion(color(white)) ///

graphregion(margin(zero)) favours(Favours intervention # Favours control) texts(105) astext(60) xlabel(-10(5)5) range(-10,5.5) noadjust ysize(3) xsize(6)) ///

: regress Change\_in\_AsBPM\_12m Allocation Age Sex CSBP\_Baseline Diabetes level\_of\_intervention if Dataset==6|Dataset==5| Dataset==7| Dataset==9

\*\*\*\*\*IPD mean change in dBP at follow-up by study, adjusted by age, sex and baseline BP\*\*\*\*\*\*\*\*\*\*\*\*

\*Clinic 6 mths

set more off

ipdmetan, study(Study) effect(Mean dBP diff) re lcols((count) Total\_population\_6m (sum) Control\_6m Intervention\_6m) forest(graphregion(color(white)) ///

graphregion(margin(zero)) favours(Favours intervention # Favours control) texts(105) astext(60) xlabel(-5(2.5)5) range(-5.5,5.5) noadjust ysize(3) xsize(6)) ///

: regress Change\_in\_dBP\_6m Allocation Age Sex CDBP\_Baseline Diabetes level\_of\_intervention if Dataset==4|Dataset==5| Dataset==7 | Dataset==8 | Dataset==9

\*Ambulatory 6 mths

set more off

ipdmetan, study(Study) effect(Mean dBP diff) re lcols((count) Total\_population\_6m (sum) Control\_6m Intervention\_6m) forest(graphregion(color(white)) ///

graphregion(margin(zero)) favours(Favours intervention # Favours control) texts(105) astext(60) xlabel(-5(2.5)5) range(-5.5,5.5) noadjust ysize(3) xsize(6)) ///

: regress Change\_in\_AdBPM\_6m Allocation Age Sex CDBP\_Baseline Diabetes level\_of\_intervention if Dataset==4|Dataset==5| Dataset==7 | Dataset==8 | Dataset==9

\*Clinic 12 mths

set more off

ipdmetan, study(Study) effect(Mean dBP diff) re lcols((count) Total\_population\_12m (sum) Control\_12m Intervention\_12m) forest(graphregion(color(white)) ///

graphregion(margin(zero)) favours(Favours intervention # Favours control) texts(105) astext(60) xlabel(-5(2.5)5) range(-5.5,5.5) noadjust ysize(3) xsize(6)) ///

: regress Change\_in\_dBP\_12m Allocation Age Sex CDBP\_Baseline Diabetes level\_of\_intervention if Dataset==6|Dataset==5| Dataset==7 | Dataset==9

\*Ambulatory 12 mths

set more off

ipdmetan, study(Study) effect(Mean sBP diff) re lcols((count) Total\_population\_12m (sum) Control\_12m Intervention\_12m) forest(graphregion(color(white)) ///

graphregion(margin(zero)) favours(Favours intervention # Favours control) texts(105) astext(60) xlabel(-5(2.5)5) range(-5.5,5.5) noadjust ysize(3) xsize(6)) ///

: regress Change\_in\_AdBPM\_12m Allocation Age Sex CDBP\_Baseline Diabetes level\_of\_intervention if Dataset==6|Dataset==5| Dataset==7 | Dataset==9

\*\*\*\*\*\*\*Sub-group analyses\*\*\*\*\*\*\*

\*\*\*\*\*IPD mean change in sBP at 12months by age, adjusted by sex, and baseline BP and level of intervention\*\*\*\*\*\*\*\*\*\*\*\*

use "G:\SMART BP IPD\Pooled analysis\BPSMART dataset\_subgroup.dta", clear

set more off

ipdmetan, study(Subgroup\_category) by(Subgroup) effect(Mean sBP diff) re lcols(Total\_studies (count) Complete\_data (sum) Complete\_data\_Con Complete\_data\_Int ) ///

forest(graphregion(color(white)) graphregion(margin(zero)) favours(Favours intervention # Favours control) texts(105) astext(60) xlabel(-15(5)5) range(-13,5) boxsca(50) ///

ysize(6) xsize(5.5) boxopts(msymbol(D))) nooverall nosubgroup: regress Change\_in\_sBP\_12m Allocation Age Sex CSBP\_Baseline i.level\_of\_intervention i.study\_variable ///

if Dataset\_ID==1 | Dataset\_ID==2 | Dataset\_ID==3 | Dataset\_ID==6 | Dataset\_ID==5 | Dataset\_ID==7| Dataset\_ID==9 | Dataset\_ID==10 | Dataset\_ID==16 ///

| Dataset\_ID==121 | Dataset\_ID==122 | Dataset\_ID==141 | Dataset\_ID==142 | Dataset\_ID==191 | Dataset\_ID==192 | Dataset\_ID==131 ///

| Dataset\_ID==132 | Dataset\_ID==133 | Dataset\_ID==20

\*\*\*\*\*IPD mean change in dBP at 12months by age, adjusted by sex, and baseline BP and level of intervention\*\*\*\*\*\*\*\*\*\*\*\*

use "G:\SMART BP IPD\Pooled analysis\BPSMART dataset\_subgroup.dta", clear

set more off

ipdmetan, study(Subgroup\_category) by(Subgroup) effect(Mean dBP diff) re lcols(Total\_studies (count) Complete\_data (sum) Complete\_data\_Con Complete\_data\_Int ) ///

forest(graphregion(color(white)) graphregion(margin(zero)) favours(Favours intervention # Favours control) texts(105) astext(60) xlabel(-10(5)5) range(-10,5) boxsca(50) ///

ysize(6) xsize(5.5) boxopts(msymbol(D))) nooverall nosubgroup : regress Change\_in\_dBP\_12m Allocation Age Sex CDBP\_Baseline i.level\_of\_intervention i.study\_variable ///

if Dataset\_ID==1 | Dataset\_ID==2 | Dataset\_ID==3 | Dataset\_ID==6 | Dataset\_ID==5 | Dataset\_ID==7| Dataset\_ID==9 | Dataset\_ID==10 | Dataset\_ID==16 ///

| Dataset\_ID==121 | Dataset\_ID==122 | Dataset\_ID==141 | Dataset\_ID==142 | Dataset\_ID==191 | Dataset\_ID==192 | Dataset\_ID==131 ///

| Dataset\_ID==132 | Dataset\_ID==133 | Dataset\_ID==20

\*\*\*RR of BP control by study, adjusted by age, sex, Diabetes and baseline BP\*\*\*\*\*\*\*\*\*\*

use "G:\SMART BP IPD\Pooled analysis\BPSMART dataset\_subgroup.dta", clear

set more off

recode BP\_control\_12m (1=2)

recode BP\_control\_12m (0=1)

recode BP\_control\_12m (2=0)

ipdmetan, study(Subgroup\_category) by(Subgroup) effect(RR of BP control) re lcols(Total\_studies (count) Complete\_data (sum) Complete\_data\_Con Complete\_data\_Int) ///

forest(graphregion(color(white)) graphregion(margin(zero)) favours(Favours intervention # Favours control) texts(100) astext(60) xlabel(0.5(0.5)1.5) range(0.1,2) boxsca(35) ///

ysize(6) xsize(5.5) boxopts(msymbol(D))) nooverall nosubgroup rrr : mlogit BP\_control\_12m Allocation Age Sex CSBP\_Baseline CDBP\_Baseline i.level\_of\_intervention i.study\_variable ///

if Dataset\_ID==1 | Dataset\_ID==2 | Dataset\_ID==3 | Dataset\_ID==6 | Dataset\_ID==5 | Dataset\_ID==7| Dataset\_ID==9 | Dataset\_ID==10 | Dataset\_ID==16 ///

| Dataset\_ID==121 | Dataset\_ID==122 | Dataset\_ID==141 | Dataset\_ID==142 | Dataset\_ID==191 | Dataset\_ID==192 | Dataset\_ID==131 ///

| Dataset\_ID==132 | Dataset\_ID==133 | Dataset\_ID==20, baseoutcome(0)