CODE USING STATA16 for manuscript: Lind et al: .

**PLASMA PROTEIN PROFILE OF CAROTID ARTERY ATHEROSCLEROSIS AND ATHEROSCLEROTIC OUTCOMES**

**- META-ANALYSES AND MENDELIAN RANDOMIZATION ANALYSES**

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\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*PIVUS

clear

cd "/Users/larslind/"

use "Lind kopior/Proteomics/PIVUS data proteomics70\_korr.dta"

sort lpnr

merge lpnr using "Lind kopior/PIVUS pek tander vs athero/PIVUS pek tander vs athero6.dta"

sum \_merge

drop \_merge

egen area=rowtotal(areadx areasin), missing

gen lnarea=log(area)

gen lnimtcca=log(imtfmeansindx2)

gen lnimtbulb=log(bulbimtfmeandxsin)

egen plaquegsm=rowmean(areadx areasin)

corr lnimtcca lnimtbulb

tw (scatter lnimtcca lnimtbulb) (qfit lnimtcca lnimtbulb), aspect(1)

\*gen anyplaque=nrofarterieswithplaque

\*recode anyplaque (2=1)

tab anyplaque

gen plaque=.

replace plaque=0 if imtfmeansindx2!=.

replace plaque=1 if imtfmeansindx2!=. & imtfmeansindx2>=1.2

replace plaque=1 if imtfmeansindx2!=. & bulbimtfmeandxsin>=1.2 & bulbimtfmeandxsin!=.

tab plaque

gen age=70

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*basic table

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

file open table1 using "basic table\_PIVUS.txt", replace write

file write table1 "Variable" \_tab "n" \_tab "Mean" \_tab "SD" \_n

foreach var of varlist age kn manuelltsbp hdl ldl bmi diabetesmellitus rkarenu imtfmeansindx2 bulbimtfmeandxsin anyplaque area plaquegsm {

quietly: sum `var' if imtfmeansindx2!=.

file write table1 "`var'" \_tab (r(N)) \_tab (round(r(mean),0.01)) \_tab (round(r(sd),0.01)) \_n

}

file close table1

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*. IMT CCA

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

file open table2 using "Table proteomics vs IMTCCA.txt", replace write

file write table2 "Variable" \_tab "n1" \_tab "Beta1" \_tab "SE1" \_tab "CIlower1" \_tab "CIhigher1" \_tab "P-value1" \_tab \_tab "n2" \_tab "Beta2" \_tab "SE2" \_tab "CIlower2" \_tab "CIhigher2" \_tab "P-value2" \_n // två st för CI

foreach var of varlist prot\* {

quietly: reg lnimtcca `var' age kn lpnr

file write table2 "`var'" \_tab (e(N)) \_tab %5.3f (\_b[`var']) \_tab %5.3f (\_se[`var']) \_tab %5.3f (\_b[`var']-1.96\*\_se[`var']) \_tab %5.3f (\_b[`var']+1.96\*\_se[`var']) \_tab %12.10f (round(2\*(ttail(e(df\_r),abs(\_b[`var']/\_se[`var']))),0.000000000000001)) \_tab

quietly: reg lnimtcca `var' age kn manuelltsbp hdl ldl bmi diabetesmellitus rkarenu lpnr

file write table2 \_tab (e(N)) \_tab %5.3f (\_b[`var']) \_tab %5.3f (\_se[`var']) \_tab %5.3f (\_b[`var']-1.96\*\_se[`var']) \_tab %5.3f (\_b[`var']+1.96\*\_se[`var']) \_tab %12.10f (round(2\*(ttail(e(df\_r),abs(\_b[`var']/\_se[`var']))),0.000000000000001)) \_n

}

file close table2

\*tabell alla

clear

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

insheet using "Table proteomics vs IMTCCA.txt"

sort variable

merge variable using "/Users/larslind/Lind kopior/Proteomics/proteinnamn\_korr.dta"

tab \_merge

drop if \_merge!=3

drop \_merge

sort pvalue1

keep proteinname n1 beta1 se1 cilower1 cihigher1 pvalue1 n2 beta2 se2 cilower2 cihigher2 pvalue2

order proteinname n1 beta1 se1 cilower1 cihigher1 pvalue1 n2 beta2 se2 cilower2 cihigher2 pvalue2

sort proteinname

save "Table proteomics vs IMTCCA\_PIVUS.dta", replace

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*. IMT bulb

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

file open table2 using "Table proteomics vs IMTbulb.txt", replace write

file write table2 "Variable" \_tab "n1" \_tab "Beta1" \_tab "SE1" \_tab "CIlower1" \_tab "CIhigher1" \_tab "P-value1" \_tab \_tab "n2" \_tab "Beta2" \_tab "SE2" \_tab "CIlower2" \_tab "CIhigher2" \_tab "P-value2" \_n // två st för CI

foreach var of varlist prot\* {

quietly: reg lnimtbulb `var' age kn lpnr

file write table2 "`var'" \_tab (e(N)) \_tab %5.3f (\_b[`var']) \_tab %5.3f (\_se[`var']) \_tab %5.3f (\_b[`var']-1.96\*\_se[`var']) \_tab %5.3f (\_b[`var']+1.96\*\_se[`var']) \_tab %12.10f (round(2\*(ttail(e(df\_r),abs(\_b[`var']/\_se[`var']))),0.000000000000001)) \_tab

quietly: reg lnimtbulb `var' age kn manuelltsbp hdl ldl bmi diabetesmellitus rkarenu lpnr

file write table2 \_tab (e(N)) \_tab %5.3f (\_b[`var']) \_tab %5.3f (\_se[`var']) \_tab %5.3f (\_b[`var']-1.96\*\_se[`var']) \_tab %5.3f (\_b[`var']+1.96\*\_se[`var']) \_tab %12.10f (round(2\*(ttail(e(df\_r),abs(\_b[`var']/\_se[`var']))),0.000000000000001)) \_n

}

file close table2

\*tabell alla

clear

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

insheet using "Table proteomics vs IMTbulb.txt"

sort variable

merge variable using "/Users/larslind/Lind kopior/Proteomics/proteinnamn\_korr.dta"

tab \_merge

drop if \_merge!=3

drop \_merge

sort pvalue1

keep proteinname n1 beta1 se1 cilower1 cihigher1 pvalue1 n2 beta2 se2 cilower2 cihigher2 pvalue2

order proteinname n1 beta1 se1 cilower1 cihigher1 pvalue1 n2 beta2 se2 cilower2 cihigher2 pvalue2

sort proteinname

save "Table proteomics vs IMTbulb\_PIVUS.dta", replace

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*. plaque area

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

file open table2 using "Table proteomics vs area.txt", replace write

file write table2 "Variable" \_tab "n1" \_tab "Beta1" \_tab "SE1" \_tab "CIlower1" \_tab "CIhigher1" \_tab "P-value1" \_tab \_tab "n2" \_tab "Beta2" \_tab "SE2" \_tab "CIlower2" \_tab "CIhigher2" \_tab "P-value2" \_n // två st för CI

foreach var of varlist prot\* {

quietly: reg lnarea `var' age kn lpnr

file write table2 "`var'" \_tab (e(N)) \_tab %5.3f (\_b[`var']) \_tab %5.3f (\_se[`var']) \_tab %5.3f (\_b[`var']-1.96\*\_se[`var']) \_tab %5.3f (\_b[`var']+1.96\*\_se[`var']) \_tab %12.10f (round(2\*(ttail(e(df\_r),abs(\_b[`var']/\_se[`var']))),0.000000000000001)) \_tab

quietly: reg lnarea `var' age kn manuelltsbp hdl ldl bmi diabetesmellitus rkarenu lpnr

file write table2 \_tab (e(N)) \_tab %5.3f (\_b[`var']) \_tab %5.3f (\_se[`var']) \_tab %5.3f (\_b[`var']-1.96\*\_se[`var']) \_tab %5.3f (\_b[`var']+1.96\*\_se[`var']) \_tab %12.10f (round(2\*(ttail(e(df\_r),abs(\_b[`var']/\_se[`var']))),0.000000000000001)) \_n

}

file close table2

\*tabell alla

clear

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

insheet using "Table proteomics vs area.txt"

sort variable

merge variable using "/Users/larslind/Lind kopior/Proteomics/proteinnamn\_korr.dta"

tab \_merge

drop if \_merge!=3

drop \_merge

sort pvalue1

keep proteinname n1 beta1 se1 cilower1 cihigher1 pvalue1 n2 beta2 se2 cilower2 cihigher2 pvalue2

order proteinname n1 beta1 se1 cilower1 cihigher1 pvalue1 n2 beta2 se2 cilower2 cihigher2 pvalue2

sort proteinname

save "Table proteomics vs area\_PIVUS.dta", replace

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*. any plaque

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

file open table2 using "Table proteomics vs anyplaque.txt", replace write

file write table2 "Variable" \_tab "n1" \_tab "Beta1" \_tab "SE1" \_tab "CIlower1" \_tab "CIhigher1" \_tab "P-value1" \_tab \_tab "n2" \_tab "Beta2" \_tab "SE2" \_tab "CIlower2" \_tab "CIhigher2" \_tab "P-value2" \_n // två st för CI

foreach var of varlist prot\* {

quietly: logit anyplaque `var' age kn lpnr

file write table2 "`var'" \_tab (e(N)) \_tab %5.3f (\_b[`var']) \_tab %5.3f (\_se[`var']) \_tab %5.3f (\_b[`var']-1.96\*\_se[`var']) \_tab %5.3f (\_b[`var']+1.96\*\_se[`var']) \_tab (round(2\*(1-normal(abs(\_b[`var']/\_se[`var']))),0.0000000000001)) \_tab

quietly: logit anyplaque `var' age kn manuelltsbp hdl ldl bmi diabetesmellitus rkarenu lpnr

file write table2 \_tab (e(N)) \_tab %5.3f (\_b[`var']) \_tab %5.3f (\_se[`var']) \_tab %5.3f (\_b[`var']-1.96\*\_se[`var']) \_tab %5.3f (\_b[`var']+1.96\*\_se[`var']) \_tab (round(2\*(1-normal(abs(\_b[`var']/\_se[`var']))),0.0000000000001)) \_n

}

file close table2

\*tabell alla

clear

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

insheet using "Table proteomics vs anyplaque.txt"

sort variable

merge variable using "/Users/larslind/Lind kopior/Proteomics/proteinnamn\_korr.dta"

tab \_merge

drop if \_merge!=3

drop \_merge

sort pvalue1

keep proteinname n1 beta1 se1 cilower1 cihigher1 pvalue1 n2 beta2 se2 cilower2 cihigher2 pvalue2

order proteinname n1 beta1 se1 cilower1 cihigher1 pvalue1 n2 beta2 se2 cilower2 cihigher2 pvalue2

sort proteinname

save "Table proteomics vs anyplaque\_PIVUS.dta", replace

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* POEM

clear

use "/Users/larslind/Lind kopior/POEM/POEM datafiler/POEM data basalfil\_CF.dta"

sort lpnr

merge lpnr using "/Users/larslind/Lind kopior/POEM/POEM datafiler/POEM data protomics\_CF.dta"

tab \_merge

drop \_merge

sort lpnr

merge lpnr using "/Users/larslind/Lind kopior/POEM/POEM datafiler/POEM data IMT and IM\_GSM.dta"

tab \_merge

drop \_merge

gen lnimtcca=log(imt)

foreach var of varlist \_il8 - \_ecp {

egen `var'SD=std(`var')

}

gen age=50

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*basic table

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

file open table1 using "basic table\_POEM.txt", replace write

file write table1 "Variable" \_tab "n" \_tab "Mean" \_tab "SD" \_n

foreach var of varlist age kn manuelltsbp hdl ldl bmi diabetesmellitus rkarenu imt {

quietly: sum `var' if imt!=.

file write table1 "`var'" \_tab (r(N)) \_tab (round(r(mean),0.01)) \_tab (round(r(sd),0.01)) \_n

}

file close table1

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*. IMT CCA

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

file open table2 using "Table proteomics vs IMTCCA\_POEM.txt", replace write

file write table2 "Variable" \_tab "n1" \_tab "Beta1" \_tab "SE1" \_tab "CIlower1" \_tab "CIhigher1" \_tab "P-value1" \_tab \_tab "n2" \_tab "Beta2" \_tab "SE2" \_tab "CIlower2" \_tab "CIhigher2" \_tab "P-value2" \_n // två st för CI

foreach var of varlist \_il8SD - \_ecpSD {

quietly: reg lnimtcca `var' age kn lpnr

file write table2 "`var'" \_tab (e(N)) \_tab %5.3f (\_b[`var']) \_tab %5.3f (\_se[`var']) \_tab %5.3f (\_b[`var']-1.96\*\_se[`var']) \_tab %5.3f (\_b[`var']+1.96\*\_se[`var']) \_tab %12.10f (round(2\*(ttail(e(df\_r),abs(\_b[`var']/\_se[`var']))),0.000000000000001)) \_tab

quietly: reg lnimtcca `var' age kn manuelltsbp hdl ldl bmi diabetesmellitus rkarenu lpnr

file write table2 \_tab (e(N)) \_tab %5.3f (\_b[`var']) \_tab %5.3f (\_se[`var']) \_tab %5.3f (\_b[`var']-1.96\*\_se[`var']) \_tab %5.3f (\_b[`var']+1.96\*\_se[`var']) \_tab %12.10f (round(2\*(ttail(e(df\_r),abs(\_b[`var']/\_se[`var']))),0.000000000000001)) \_n

}

file close table2

\*tabell alla

clear

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

insheet using "Table proteomics vs IMTCCA\_POEM.txt"

ren variable variable\_poem

sort variable\_poem

merge variable\_poem using "/Users/larslind/Lind kopior/Proteomics/proteinnamn\_poem\_long analysis.dta"

tab \_merge

drop if \_merge!=3

drop \_merge

sort pvalue1

keep proteinname n1 beta1 se1 cilower1 cihigher1 pvalue1 n2 beta2 se2 cilower2 cihigher2 pvalue2

order proteinname n1 beta1 se1 cilower1 cihigher1 pvalue1 n2 beta2 se2 cilower2 cihigher2 pvalue2

sort proteinname

save "Table proteomics vs IMTCCA\_POEM.dta", replace

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* MDC

\*IMT\_CCA

clear

import delimited "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/IMTCCA\_MDC.txt", encoding(ISO-8859-1)clear

sort pvalue

gen radnummer=\_n

gen vv3= 0.05\*(radnummer/88) // två outcomes

gen FDRyes=0

replace FDRyes=1 if pvalue <vv3

keep if FDRyes==1

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/IMTCCA\_MDC\_FDRpos.dta", replace

keep protein

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/IMTCCA\_MDC\_FDRpos\_proteinname.dta", replace

clear

import delimited "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/IMTCCA\_MDC.txt", encoding(ISO-8859-1)clear

ren protein proteinname

ren n n1

ren beta beta1

ren se se1

ren cilower cilower1

ren cihigher cihigher1

ren pvalue pvalue1

drop v8

ren v9 n2

ren v10 beta2

ren v11 se2

ren v12 cilower2

ren v13 cihigher2

ren v14 pvalue2

gen study="MDC"

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTCCA\_MDC.dta", replace

\*Plaque

clear

import delimited "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Plaque\_MDC.txt", encoding(ISO-8859-1)clear

sort pvalue

gen radnummer=\_n

gen vv3= 0.05\*(radnummer/88) // två outcomes

gen FDRyes=0

replace FDRyes=1 if pvalue <vv3

keep if FDRyes==1

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Plaque\_MDC\_FDRpos.dta", replace

keep protein

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Plaque\_MDC\_FDRpos\_proteinname.dta", replace

clear

import delimited "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Plaque\_MDC.txt", encoding(ISO-8859-1)clear

ren protein proteinname

ren n n1

ren beta beta1

ren se se1

ren cilower cilower1

ren cihigher cihigher1

ren pvalue pvalue1

drop v8

ren v9 n2

ren v10 beta2

ren v11 se2

ren v12 cilower2

ren v13 cihigher2

ren v14 pvalue2

gen study="MDC"

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs anyplaque\_MDC.dta", replace

\*IMTbulb

clear

import delimited "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/IMTbulb\_MDC.txt", encoding(ISO-8859-1)clear

sort pvalue

gen radnummer=\_n

gen vv3= 0.05\*(radnummer/88) // två outcomes

gen FDRyes=0

replace FDRyes=1 if pvalue <vv3

keep if FDRyes==1

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/IMTbulb\_MDC\_FDRpos.dta", replace

keep protein

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/IMTbulb\_MDC\_FDRpos\_proteinname.dta", replace

clear

import delimited "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/IMTbulb\_MDC.txt", encoding(ISO-8859-1)clear

ren protein proteinname

ren n n1

ren beta beta1

ren se se1

ren cilower cilower1

ren cihigher cihigher1

ren pvalue pvalue1

drop v8

ren v9 n2

ren v10 beta2

ren v11 se2

ren v12 cilower2

ren v13 cihigher2

ren v14 pvalue2

gen study="MDC"

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTbulb\_MDC.dta", replace

\*\*\*\*\*\*\*\*\*\*\* CARDIPP

\*imt

\*import delimited "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Results\_metaanalysis for proteins vs IMTCCA\_CARDIPP.txt", encoding(ISO-8859-1) clear

import delimited "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTCCA\_SAVAcontrol.txt", encoding(ISO-8859-1) clear

\*import delimited "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTCCA\_SAVA\_PADVA.txt", encoding(ISO-8859-1) clear

ren protein proteinname

ren n n1

ren beta beta1

ren se se1

ren cilower cilower1

ren cihigher cihigher1

ren pvalue pvalue1

drop v8

ren v9 n2

ren v10 beta2

ren v11 se2

ren v12 cilower2

ren v13 cihigher2

ren v14 pvalue2

\*save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTCCA\_CARDIPP.dta", replace

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTCCA\_SAVAcontrol.dta", replace

\*save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTCCA\_SAVA\_PADVA.dta", replace

\*plaque

\*import delimited "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs anyplaque\_CARDIPP.txt", encoding(ISO-8859-1) clear

\*import delimited "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs anyplaque\_SAVAcontrol.txt", encoding(ISO-8859-1) clear

import delimited "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs anyplaque\_SAVA\_PADVA.txt", encoding(ISO-8859-1) clear

ren protein proteinname

ren n n1

ren beta beta1

ren se se1

ren cilower cilower1

ren cihigher cihigher1

ren pvalue pvalue1

drop v8

ren v9 n2

ren v10 beta2

ren v11 se2

ren v12 cilower2

ren v13 cihigher2

ren v14 pvalue2

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs anyplaque\_CARDIPP.dta", replace

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs anyplaque\_SAVAcontrol.dta", replace

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs anyplaque\_SAVA\_PADVA.dta", replace

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*IMPROVE

\*imt CCA

import delimited "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/IMT\_CCA\_IMPROVE.txt", encoding(ISO-8859-1) clear

ren protein proteinname

ren n n1

ren beta beta1

ren se se1

ren cilower cilower1

ren cihigher cihigher1

ren pvalue pvalue1

\*drop v8

ren v8 n2

ren v9 beta2

ren v10 se2

ren v11 cilower2

ren v12 cihigher2

ren v13 pvalue2

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTCCA\_IMPROVE.dta", replace

\*omkörning

import delimited "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/IMT\_CCA\_IMPROVE\_utan log.txt", encoding(ISO-8859-1) clear

ren protein proteinname

ren n n1

ren beta beta1

ren se se1

ren cilower cilower1

ren cihigher cihigher1

ren pvalue pvalue1

\*drop v8

ren v8 n2

ren v9 beta2

ren v10 se2

ren v11 cilower2

ren v12 cihigher2

ren v13 pvalue2

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTCCA\_IMPROVE\_utan log.dta", replace

\*imt bulb

import delimited "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/IMT\_Bulb\_IMPROVE.txt", encoding(ISO-8859-1) clear

ren protein proteinname

ren n n1

ren beta beta1

ren se se1

ren cilower cilower1

ren cihigher cihigher1

ren pvalue pvalue1

drop v8

ren v9 n2

ren v10 beta2

ren v11 se2

ren v12 cilower2

ren v13 cihigher2

ren v14 pvalue2

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTBulb\_IMPROVE.dta", replace

\*omkörning

import delimited "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/IMT\_Bulb\_IMPROVE\_utan log.txt", encoding(ISO-8859-1) clear

ren protein proteinname

ren n n1

ren beta beta1

ren se se1

ren cilower cilower1

ren cihigher cihigher1

ren pvalue pvalue1

drop v8

ren v9 n2

ren v10 beta2

ren v11 se2

ren v12 cilower2

ren v13 cihigher2

ren v14 pvalue2

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTBulb\_IMPROVE\_utan log.dta", replace

\*plaque

import delimited "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Plaque\_IMPROVE.txt", encoding(ISO-8859-1) clear

ren protein proteinname

ren n n1

ren beta beta1

ren se se1

ren cilower cilower1

ren cihigher cihigher1

ren pvalue pvalue1

drop v8

ren v9 n2

ren v10 beta2

ren v11 se2

ren v12 cilower2

ren v13 cihigher2

ren v14 pvalue2

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs anyplaque\_IMPROVE.dta", replace

\*\*\*\*Göra iodrning dataset inför metaanalysen

\*imt

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTCCA\_PIVUS.dta", replace

gen study="PIVUS"

save, replace

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTCCA\_POEM.dta", replace

gen study="POEM"

save, replace

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTCCA\_CARDIPP.dta", replace

gen study="CARDIPP"

save, replace

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTCCA\_SAVAcontrol.dta", replace

gen study="SAVAcontrol"

save, replace

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTCCA\_SAVA\_PADVA.dta", replace

gen study="SAVA\_PADVA"

save, replace

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTCCA\_IMPROVE\_utan log.dta", replace

gen study="IMPROVE"

save, replace

\*plaque

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs anyplaque\_PIVUS.dta", replace

gen study="PIVUS"

save, replace

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs anyplaque\_CARDIPP.dta", replace

gen study="CARDIPP"

save, replace

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs anyplaque\_SAVAcontrol.dta", replace

gen study="SAVAcontrol"

save, replace

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs anyplaque\_SAVA\_PADVA.dta", replace

gen study="SAVA\_PADVA"

save, replace

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs anyplaque\_IMPROVE.dta", replace

gen study="IMPROVE"

save, replace

\*IMTbulb

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTbulb\_PIVUS.dta", replace

gen study="PIVUS"

save, replace

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTBulb\_IMPROVE\_utan log.dta", replace

gen study="IMPROVE"

save, replace

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* META-analys IMTCCA

\*ojusterat

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTCCA\_PIVUS.dta"

append using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTCCA\_POEM.dta"

append using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTCCA\_CARDIPP.dta"

append using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTCCA\_SAVAcontrol.dta"

append using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTCCA\_SAVA\_PADVA.dta"

append using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTCCA\_IMPROVE.dta"

sort proteinname

ren pvalue1 p

ren proteinname met

ren se1 se

ren beta1 beta

levelsof met, local(levels)

foreach l of local levels {

di "`l'"

}

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

file open a using "metaresultat\_IMTCCA\_unadj.txt", replace write

file write a "met" \_tab "beta" \_tab "se" \_tab "p" \_tab "I\_sq" \_n

foreach l of local levels {

metan beta se if met=="`l'", nograph fixedi

file write a "`l'" \_tab (r(ES)) \_tab (r(seES)) \_tab (2\*normal(-abs((r(ES))/(r(seES))))) \_tab (r(i\_sq)) \_n

}

file close a

clear

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

insheet using "metaresultat\_IMTCCA\_unadj.txt"

ren met protein

ren beta beta1

ren se se1

ren p p1

ren i\_sq i\_sq1

sort protein

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/metaresultat\_IMTCCA\_unadj.dta", replace

\*adjusted

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTCCA\_PIVUS.dta"

append using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTCCA\_POEM.dta"

append using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTCCA\_CARDIPP.dta"

append using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTCCA\_SAVAcontrol.dta"

append using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTCCA\_SAVA\_PADVA.dta"

append using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTCCA\_IMPROVE.dta"

sort proteinname

ren pvalue2 p

ren proteinname met

ren se2 se

ren beta2 beta

levelsof met, local(levels)

foreach l of local levels {

di "`l'"

}

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

file open a using "metaresultat\_IMTCCA\_adj.txt", replace write

file write a "met" \_tab "beta" \_tab "se" \_tab "p" \_tab "I\_sq" \_n

foreach l of local levels {

metan beta se if met=="`l'", nograph fixedi

file write a "`l'" \_tab (r(ES)) \_tab (r(seES)) \_tab (2\*normal(-abs((r(ES))/(r(seES))))) \_tab (r(i\_sq)) \_n

}

file close a

clear

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

insheet using "metaresultat\_IMTCCA\_adj.txt"

ren met protein

ren beta beta2

ren se se2

ren p p2

ren i\_sq i\_sq2

sort protein

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/metaresultat\_IMTCCA\_adj.dta"

\*slå ihop till en tabell

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/metaresultat\_IMTCCA\_unadj.dta", clear

merge protein using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/metaresultat\_IMTCCA\_adj.dta"

tab \_merge

drop \_merge

sort protein

merge protein using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/IMTCCA\_MDC\_FDRpos\_proteinname.dta"

tab \_merge

drop if \_merge!=3

drop \_merge

sort p1

gen radnummer=\_n

gen vv3= 0.05\*(radnummer/63)

gen FDRyes=0

replace FDRyes=1 if p1 <vv3

keep if FDRyes==1

drop radnummer vv3 FDRyes

\* för figur IMT\_CCA- discovery

clear

import delimited "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/IMTCCA\_MDC.txt", encoding(ISO-8859-1)clear

ren protein proteinname

sort proteinname

merge proteinname using "/Users/larslind/Lind kopior/Proteomics/proteinnamn\_korr\_sorted on proteinname.dta"

drop if \_merge!=3

drop if proteinname=="Protein S100-A12 (EN-RAGE)"

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/IMTCCA\_MDC\_till figur.dta", replace

\* för figur IMT\_CCA- validation meta-analysis

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/metaresultat\_IMTCCA\_unadj.dta", clear

ren protein proteinname

sort proteinname

merge proteinname using "/Users/larslind/Lind kopior/Proteomics/proteinnamn\_korr\_sorted on proteinname.dta"

drop if \_merge!=3

drop if proteinname=="Protein S100-A12 (EN-RAGE)"

drop if proteinname=="Beta-nerve growth factor (Beta-NGF)"

drop if proteinname=="NF-kappa-B essential modulator (NEMO)"

drop if proteinname=="Natriuretic peptides B (BNP)"

drop if proteinname=="Agouti-related protein (AGRP)"

drop if proteinname=="Ovarian cancer-related tumor marker CA 125 (CA-125)"

drop if proteinname=="SIR2-like protein (SIRT2)"

ren beta1 beta

gen cilower=beta-(1.96\*se1)

gen cihigher=beta+(1.96\*se1)

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/IMTCCA\_metaanalys\_till figur.dta", replace

\* i R för discovery IMT\_CCA

library("haven")

d\_IMTCCA\_MDC <- read\_dta("/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/IMTCCA\_MDC\_till figur.dta")

d\_IMTCCA\_MDC <- d\_IMTCCA\_MDC[order(d\_IMTCCA\_MDC$beta),]

xlims\_d\_IMTCCA\_MDC <- c(min(d\_IMTCCA\_MDC$cilower) - 0.01, max(d\_IMTCCA\_MDC$cihigher) + 0.01)

ylims <- c(-0.02, nrow(d\_max) + 1) ## Måste sätta denna annars blir det fel

ycex <- 0.6 ## Storlek på y-labels

library(lattice)

plot\_d\_IMTCCA\_MDC <- with(d\_IMTCCA\_MDC,

xyplot(1:nrow(d\_IMTCCA\_MDC) ~ beta, data = d\_IMTCCA\_MDC, xlim = xlims\_d\_IMTCCA\_MDC, ylim = ylims,

panel = function(x, y, ...) {

panel.abline(v = 0, lty = 2)

panel.arrows(x0 = cilower,

y0 = y,

x1 = cihigher,

y1 = y,

code = 3, length = 0.02,

angle = 90)

panel.xyplot(x, y, pch = 16, col = "black")

}, scales = list(y = list(at = 1:nrow(d\_IMTCCA\_MDC), lab = v3,

cex = ycex, tck = c(1, 0))),

ylab = "", xlab = expression(beta), main = "IMT - CCA discovery")

)

print(plot\_d\_IMTCCA\_MDC)

\* i R för validation IMT\_CCA

library("haven")

d\_IMTCCA\_meta <- read\_dta("/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/IMTCCA\_metaanalys\_till figur.dta")

d\_IMTCCA\_meta <- d\_IMTCCA\_meta[order(d\_IMTCCA\_meta$beta),]

xlims\_d\_IMTCCA\_meta <- c(min(d\_IMTCCA\_meta$cilower) - 0.01, max(d\_IMTCCA\_meta$cihigher) + 0.01)

ylims <- c(-0.02, nrow(d\_max) + 1) ## Måste sätta denna annars blir det fel

ycex <- 0.6 ## Storlek på y-labels

library(lattice)

plot\_d\_IMTCCA\_meta <- with(d\_IMTCCA\_meta,

xyplot(1:nrow(d\_IMTCCA\_meta) ~ beta, data = d\_IMTCCA\_meta, xlim = xlims\_d\_IMTCCA\_meta, ylim = ylims,

panel = function(x, y, ...) {

panel.abline(v = 0, lty = 2)

panel.arrows(x0 = cilower,

y0 = y,

x1 = cihigher,

y1 = y,

code = 3, length = 0.02,

angle = 90)

panel.xyplot(x, y, pch = 16, col = "black")

}, scales = list(y = list(at = 1:nrow(d\_IMTCCA\_meta), lab = v3,

cex = ycex, tck = c(1, 0))),

ylab = "", xlab = expression(beta), main = "IMT - CCA validation")

)

print(plot\_d\_IMTCCA\_meta)

\* metaanlysplot i R för IMT\_CCA inkluderande även MDC

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTCCA\_PIVUS.dta"

append using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTCCA\_POEM.dta"

append using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTCCA\_CARDIPP.dta"

append using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTCCA\_SAVAcontrol.dta"

append using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTCCA\_SAVA\_PADVA.dta"

append using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTCCA\_IMPROVE.dta"

append using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTCCA\_MDC.dta"

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTCCA\_alla.dta", replace

library("metafor")

library("haven")

d\_metaCCA <- read\_dta("/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTCCA\_alla.dta")

vars <- unique(d\_metaCCA$proteinname)

labs <- c("MMP12", "GAL")

## Sätt ordningen här

## Fyra figurer på samma sida är ganska ok

## När de fyra är körda, ändra till 5:8 osv

inds <- c(47, 26)

#inds <- 1:4

par(mfrow = c(2, 1))

for (i in 1:length(inds)) {

ds <- as.data.frame(d\_metaCCA[d\_metaCCA$proteinname == vars[inds[i]],])

## I rma och forest finns många options. Kolla i hjälpfilen och ändra efter smak

f <- rma(yi = ds$beta2, sei = ds$se2, method = "FE")

forest(f, pch = 16, psize = 1.25,

slab = ds$study, main =

mlab = "Summary",

xlab = "Estimate")

text(0, length(ds$study) + 2, labs[i], font = 2,

cex = 1.3)

}

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*. META-ANALYSIS PLAQUE

\*unajusted

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs anyplaque\_PIVUS.dta"

append using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs anyplaque\_CARDIPP.dta"

append using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs anyplaque\_SAVAcontrol.dta"

append using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs anyplaque\_SAVA\_PADVA.dta"

append using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs anyplaque\_IMPROVE.dta"

\*ojusterat

sort proteinname

ren pvalue1 p

ren proteinname met

ren se1 se

ren beta1 beta

levelsof met, local(levels)

foreach l of local levels {

di "`l'"

}

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

file open a using "metaresultat\_plaque\_unadj.txt", replace write

file write a "met" \_tab "beta" \_tab "se" \_tab "p" \_tab "I\_sq" \_n

foreach l of local levels {

metan beta se if met=="`l'", nograph fixedi

file write a "`l'" \_tab (r(ES)) \_tab (r(seES)) \_tab (2\*normal(-abs((r(ES))/(r(seES))))) \_tab (r(i\_sq)) \_n

}

file close a

clear

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

insheet using "metaresultat\_plaque\_unadj.txt"

ren met protein

ren beta beta1

ren se se1

ren p p1

ren i\_sq i\_sq1

sort protein

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/metaresultat\_plaque\_unadj.dta", replace

\*adjusted

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs anyplaque\_PIVUS.dta"

append using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs anyplaque\_CARDIPP.dta"

append using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs anyplaque\_SAVAcontrol.dta"

append using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs anyplaque\_SAVA\_PADVA.dta"

append using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs anyplaque\_IMPROVE.dta"

sort proteinname

ren pvalue2 p

ren proteinname met

ren se2 se

ren beta2 beta

levelsof met, local(levels)

foreach l of local levels {

di "`l'"

}

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

file open a using "metaresultat\_anyplaque\_adj.txt", replace write

file write a "met" \_tab "beta" \_tab "se" \_tab "p" \_tab "I\_sq" \_n

foreach l of local levels {

metan beta se if met=="`l'", nograph fixedi

file write a "`l'" \_tab (r(ES)) \_tab (r(seES)) \_tab (2\*normal(-abs((r(ES))/(r(seES))))) \_tab (r(i\_sq)) \_n

}

file close a

clear

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

insheet using "metaresultat\_anyplaque\_adj.txt"

ren met protein

ren beta beta2

ren se se2

ren p p2

ren i\_sq i\_sq2

sort protein

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/metaresultat\_anyplaque\_adj.dta"

\*slå ihop till en tabell

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/metaresultat\_plaque\_unadj.dta", clear

merge protein using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/metaresultat\_anyplaque\_adj.dta"

tab \_merge

drop \_merge

drop if protein=="Protein S100-A12 (EN-RAGE)"

drop if protein=="Beta-nerve growth factor (Beta-NGF)"

drop if protein=="NF-kappa-B essential modulator (NEMO)"

drop if protein=="Natriuretic peptides B (BNP)"

drop if protein=="Agouti-related protein (AGRP)"

drop if protein=="Ovarian cancer-related tumor marker CA 125 (CA-125)"

drop if protein=="SIR2-like protein (SIRT2)"

sort protein

merge protein using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Plaque\_MDC\_FDRpos\_proteinname.dta"

tab \_merge

drop if \_merge!=3

drop \_merge

sort p1

gen radnummer=\_n

gen vv3= 0.05\*(radnummer/13)

gen FDRyes=0

replace FDRyes=1 if p1 <vv3

keep if FDRyes==1

drop radnummer vv3 FDRyes

\* för figur plaque- discovery

clear

import delimited "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/IMTCCA\_MDC.txt", encoding(ISO-8859-1)clear

ren protein proteinname

sort proteinname

merge proteinname using "/Users/larslind/Lind kopior/Proteomics/proteinnamn\_korr\_sorted on proteinname.dta"

drop if \_merge!=3

drop if proteinname=="Protein S100-A12 (EN-RAGE)"

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/IMTCCA\_MDC\_till figur.dta", replace

\* för figur plaque - validation meta-analysis

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/metaresultat\_IMTCCA\_unadj.dta", clear

ren protein proteinname

sort proteinname

merge proteinname using "/Users/larslind/Lind kopior/Proteomics/proteinnamn\_korr\_sorted on proteinname.dta"

drop if \_merge!=3

drop if proteinname=="Protein S100-A12 (EN-RAGE)"

drop if proteinname=="Beta-nerve growth factor (Beta-NGF)"

drop if proteinname=="NF-kappa-B essential modulator (NEMO)"

drop if proteinname=="Natriuretic peptides B (BNP)"

drop if proteinname=="Agouti-related protein (AGRP)"

drop if proteinname=="Ovarian cancer-related tumor marker CA 125 (CA-125)"

drop if proteinname=="SIR2-like protein (SIRT2)"

ren beta1 beta

gen cilower=beta-(1.96\*se1)

gen cihigher=beta+(1.96\*se1)

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/IMTCCA\_metaanalys\_till figur.dta", replace

\* i R för discovery plaque

library("haven")

d\_IMTCCA\_MDC <- read\_dta("/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/IMTCCA\_MDC\_till figur.dta")

d\_IMTCCA\_MDC <- d\_IMTCCA\_MDC[order(d\_IMTCCA\_MDC$beta),]

xlims\_d\_IMTCCA\_MDC <- c(min(d\_IMTCCA\_MDC$cilower) - 0.01, max(d\_IMTCCA\_MDC$cihigher) + 0.01)

ylims <- c(-0.02, nrow(d\_max) + 1) ## Måste sätta denna annars blir det fel

ycex <- 0.6 ## Storlek på y-labels

library(lattice)

plot\_d\_IMTCCA\_MDC <- with(d\_IMTCCA\_MDC,

xyplot(1:nrow(d\_IMTCCA\_MDC) ~ beta, data = d\_IMTCCA\_MDC, xlim = xlims\_d\_IMTCCA\_MDC, ylim = ylims,

panel = function(x, y, ...) {

panel.abline(v = 0, lty = 2)

panel.arrows(x0 = cilower,

y0 = y,

x1 = cihigher,

y1 = y,

code = 3, length = 0.02,

angle = 90)

panel.xyplot(x, y, pch = 16, col = "black")

}, scales = list(y = list(at = 1:nrow(d\_IMTCCA\_MDC), lab = v3,

cex = ycex, tck = c(1, 0))),

ylab = "", xlab = expression(beta), main = "IMT - CCA discovery")

)

print(plot\_d\_IMTCCA\_MDC)

\* i R för validation plaque

library("haven")

d\_IMTCCA\_meta <- read\_dta("/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/IMTCCA\_metaanalys\_till figur.dta")

d\_IMTCCA\_meta <- d\_IMTCCA\_meta[order(d\_IMTCCA\_meta$beta),]

xlims\_d\_IMTCCA\_meta <- c(min(d\_IMTCCA\_meta$cilower) - 0.01, max(d\_IMTCCA\_meta$cihigher) + 0.01)

ylims <- c(-0.02, nrow(d\_max) + 1) ## Måste sätta denna annars blir det fel

ycex <- 0.6 ## Storlek på y-labels

library(lattice)

plot\_d\_IMTCCA\_meta <- with(d\_IMTCCA\_meta,

xyplot(1:nrow(d\_IMTCCA\_meta) ~ beta, data = d\_IMTCCA\_meta, xlim = xlims\_d\_IMTCCA\_meta, ylim = ylims,

panel = function(x, y, ...) {

panel.abline(v = 0, lty = 2)

panel.arrows(x0 = cilower,

y0 = y,

x1 = cihigher,

y1 = y,

code = 3, length = 0.02,

angle = 90)

panel.xyplot(x, y, pch = 16, col = "black")

}, scales = list(y = list(at = 1:nrow(d\_IMTCCA\_meta), lab = v3,

cex = ycex, tck = c(1, 0))),

ylab = "", xlab = expression(beta), main = "IMT - CCA validation")

)

print(plot\_d\_IMTCCA\_meta)

\* metaanlysplot i R för plaque inkluderande även MDC

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs anyplaque\_PIVUS.dta"

append using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs anyplaque\_CARDIPP.dta"

append using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs anyplaque\_SAVAcontrol.dta"

append using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs anyplaque\_SAVA\_PADVA.dta"

append using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs anyplaque\_IMPROVE.dta"

append using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs anyplaque\_MDC.dta"

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs anyplaque\_alla.dta", replace

library("metafor")

library("haven")

d\_metaCCA <- read\_dta("/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs anyplaque\_alla.dta")

vars <- unique(d\_metaCCA$proteinname)

labs <- c("MMP12", "GDF-15")

## Sätt ordningen här

## Fyra figurer på samma sida är ganska ok

## När de fyra är körda, ändra till 5:8 osv

inds <- c(47, 29)

#inds <- 1:4

par(mfrow = c(2, 1))

for (i in 1:length(inds)) {

ds <- as.data.frame(d\_metaCCA[d\_metaCCA$proteinname == vars[inds[i]],])

## I rma och forest finns många options. Kolla i hjälpfilen och ändra efter smak

f <- rma(yi = ds$beta2, sei = ds$se2, method = "FE")

forest(f, pch = 16, psize = 1.25,

slab = ds$study,

mlab = "Summary",

xlab = "Estimate")

text(0, length(ds$study) + 2, labs[i], font = 2,

cex = 1.3)

}

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* CCA vs bulb

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*CCA

\*ojusterat

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTCCA\_PIVUS.dta"

append using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTCCA\_IMPROVE\_utan log.dta"

append using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTCCA\_MDC.dta"

sort proteinname

replace proteinname="Adrenomedullin (AM)" if proteinname=="Adrenomedullin (AM) "

replace proteinname="Agouti-related protein (AGRP)" if proteinname=="Agouti-related protein (AGRP) "

replace proteinname="Chitinase-3-like protein 1 (CHI3L1)" if proteinname=="Chitinase-3-like protein 1 (CHI3L1) "

replace proteinname="Interleukin-8 (IL-8)" if proteinname=="Interleukin-8 (IL-8) "

replace proteinname="Lectin-like oxidized LDL receptor 1 (LOX-1)" if proteinname=="Lectin-like oxidized LDL receptor 1 (LOX-1) "

replace proteinname="Matrix metalloproteinase-12 (MMP-12)" if proteinname=="Matrix metalloproteinase-12 (MMP-12) "

replace proteinname="Membrane-bound aminopeptidase P (mAmP)" if proteinname=="Membrane-bound aminopeptidase P (mAmP) "

replace proteinname="Monocyte chemotactic protein 1 (MCP-1)" if proteinname=="Monocyte chemotactic protein 1 (MCP-1) "

replace proteinname="N-terminal pro-B-type natriuretic peptide (NT-pro-BNP)" if proteinname=="N-terminal pro-B-type natriuretic peptide (NT-pro-BNP) "

replace proteinname="P-selectin glycoprotein ligand 1 (PSGL-1)" if proteinname=="P-selectin glycoprotein ligand 1 (PSGL-1) "

replace proteinname="Placenta growth factor (PlGF)" if proteinname=="Placenta growth factor (PlGF) "

replace proteinname="Prolactin (PRL)" if proteinname=="Prolactin (PRL) "

replace proteinname="Resistin (RETN)" if proteinname=="Resistin (RETN) "

replace proteinname="Thrombomodulin (TM)" if proteinname=="Thrombomodulin "

replace proteinname="Vascular endothelial growth factor A (VEGF-A)" if proteinname=="Vascular endothelial growth factor A (VEGF-A) "

replace proteinname="Vascular endothelial growth factor D (VEGF-D)" if proteinname=="Vascular endothelial growth factor D (VEGF-D) "

ren pvalue1 p

ren proteinname met

ren se1 se

ren beta1 beta

levelsof met, local(levels)

foreach l of local levels {

di "`l'"

}

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

file open a using "metaresultat\_IMTCCA\_unadj\_medMDC\_utan log.txt", replace write

file write a "met" \_tab "beta" \_tab "se" \_tab "p" \_tab "I\_sq" \_n

foreach l of local levels {

metan beta se if met=="`l'", nograph fixedi

file write a "`l'" \_tab (r(ES)) \_tab (r(seES)) \_tab (2\*normal(-abs((r(ES))/(r(seES))))) \_tab (r(i\_sq)) \_n

}

file close a

clear

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

insheet using "metaresultat\_IMTCCA\_unadj\_medMDC\_utan log.txt"

ren met protein

ren beta beta1

ren se se1

ren p p1

ren i\_sq i\_sq1

sort protein

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/metaresultat\_IMTCCA\_unadj\_medMDC\_utan log.dta", replace

\*adjusted

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTCCA\_PIVUS.dta"

append using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTCCA\_IMPROVE\_utan log.dta"

append using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTCCA\_MDC.dta"

sort proteinname

replace proteinname="Adrenomedullin (AM)" if proteinname=="Adrenomedullin (AM) "

replace proteinname="Agouti-related protein (AGRP)" if proteinname=="Agouti-related protein (AGRP) "

replace proteinname="Chitinase-3-like protein 1 (CHI3L1)" if proteinname=="Chitinase-3-like protein 1 (CHI3L1) "

replace proteinname="Interleukin-8 (IL-8)" if proteinname=="Interleukin-8 (IL-8) "

replace proteinname="Lectin-like oxidized LDL receptor 1 (LOX-1)" if proteinname=="Lectin-like oxidized LDL receptor 1 (LOX-1) "

replace proteinname="Matrix metalloproteinase-12 (MMP-12)" if proteinname=="Matrix metalloproteinase-12 (MMP-12) "

replace proteinname="Membrane-bound aminopeptidase P (mAmP)" if proteinname=="Membrane-bound aminopeptidase P (mAmP) "

replace proteinname="Monocyte chemotactic protein 1 (MCP-1)" if proteinname=="Monocyte chemotactic protein 1 (MCP-1) "

replace proteinname="N-terminal pro-B-type natriuretic peptide (NT-pro-BNP)" if proteinname=="N-terminal pro-B-type natriuretic peptide (NT-pro-BNP) "

replace proteinname="P-selectin glycoprotein ligand 1 (PSGL-1)" if proteinname=="P-selectin glycoprotein ligand 1 (PSGL-1) "

replace proteinname="Placenta growth factor (PlGF)" if proteinname=="Placenta growth factor (PlGF) "

replace proteinname="Prolactin (PRL)" if proteinname=="Prolactin (PRL) "

replace proteinname="Resistin (RETN)" if proteinname=="Resistin (RETN) "

replace proteinname="Thrombomodulin (TM)" if proteinname=="Thrombomodulin "

replace proteinname="Vascular endothelial growth factor A (VEGF-A)" if proteinname=="Vascular endothelial growth factor A (VEGF-A) "

replace proteinname="Vascular endothelial growth factor D (VEGF-D)" if proteinname=="Vascular endothelial growth factor D (VEGF-D) "

ren pvalue2 p

ren proteinname met

ren se2 se

ren beta2 beta

levelsof met, local(levels)

foreach l of local levels {

di "`l'"

}

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

file open a using "metaresultat\_IMTCCA\_adj\_medMDC\_utan log.txt", replace write

file write a "met" \_tab "beta" \_tab "se" \_tab "p" \_tab "I\_sq" \_n

foreach l of local levels {

metan beta se if met=="`l'", nograph fixedi

file write a "`l'" \_tab (r(ES)) \_tab (r(seES)) \_tab (2\*normal(-abs((r(ES))/(r(seES))))) \_tab (r(i\_sq)) \_n

}

file close a

clear

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

insheet using "metaresultat\_IMTCCA\_adj\_medMDC\_utan log.txt"

ren met protein

ren beta beta2

ren se se2

ren p p2

ren i\_sq i\_sq2

sort protein

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/metaresultat\_IMTCCA\_adj\_medMDC\_utan log.dta", replace

\*slå ihop till en tabell

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/metaresultat\_IMTCCA\_unadj\_medMDC\_utan log.dta", clear

merge protein using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/metaresultat\_IMTCCA\_adj\_medMDC\_utan log.dta"

tab \_merge

drop if \_merge!=3

drop \_merge

drop if protein=="Zscore: 169\_ITGB1BP2"

drop if protein=="Zscore: 172\_SIRT2"

drop if protein=="Zscore: 192\_NEMO"

drop if protein=="Protein S100-A12 (EN-RAGE)"

drop if protein=="Beta-nerve growth factor (Beta-NGF)"

drop if protein=="NF-kappa-B essential modulator (NEMO)"

drop if protein=="Natriuretic peptides B (BNP)"

drop if protein=="Agouti-related protein (AGRP)"

drop if protein=="Ovarian cancer-related tumor marker CA 125 (CA-125)"

drop if protein=="SIR2-like protein (SIRT2)"

gen cilower1=beta1-(1.96\*se1)

gen cihigher1=beta1+(1.96\*se1)

gen cilower2=beta2-(1.96\*se2)

gen cihigher2=beta2+(1.96\*se2)

sort p1

drop i\_sq1 i\_sq2

order protein beta1 cilower1 cihigher1 p1 beta2 cilower2 cihigher2 p2

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/metaresultat\_IMTCCA\_medMDC\_till fig\_utan log.dta", replace

\*till figur i R

\*\*CCA

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTCCA\_PIVUS.dta"

append using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTCCA\_IMPROVE\_utan log.dta"

append using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTCCA\_MDC.dta"

sort proteinname

replace proteinname="Adrenomedullin (AM)" if proteinname=="Adrenomedullin (AM) "

replace proteinname="Agouti-related protein (AGRP)" if proteinname=="Agouti-related protein (AGRP) "

replace proteinname="Chitinase-3-like protein 1 (CHI3L1)" if proteinname=="Chitinase-3-like protein 1 (CHI3L1) "

replace proteinname="Interleukin-8 (IL-8)" if proteinname=="Interleukin-8 (IL-8) "

replace proteinname="Lectin-like oxidized LDL receptor 1 (LOX-1)" if proteinname=="Lectin-like oxidized LDL receptor 1 (LOX-1) "

replace proteinname="Matrix metalloproteinase-12 (MMP-12)" if proteinname=="Matrix metalloproteinase-12 (MMP-12) "

replace proteinname="Membrane-bound aminopeptidase P (mAmP)" if proteinname=="Membrane-bound aminopeptidase P (mAmP) "

replace proteinname="Monocyte chemotactic protein 1 (MCP-1)" if proteinname=="Monocyte chemotactic protein 1 (MCP-1) "

replace proteinname="N-terminal pro-B-type natriuretic peptide (NT-pro-BNP)" if proteinname=="N-terminal pro-B-type natriuretic peptide (NT-pro-BNP) "

replace proteinname="P-selectin glycoprotein ligand 1 (PSGL-1)" if proteinname=="P-selectin glycoprotein ligand 1 (PSGL-1) "

replace proteinname="Placenta growth factor (PlGF)" if proteinname=="Placenta growth factor (PlGF) "

replace proteinname="Prolactin (PRL)" if proteinname=="Prolactin (PRL) "

replace proteinname="Resistin (RETN)" if proteinname=="Resistin (RETN) "

replace proteinname="Thrombomodulin (TM)" if proteinname=="Thrombomodulin "

replace proteinname="Vascular endothelial growth factor A (VEGF-A)" if proteinname=="Vascular endothelial growth factor A (VEGF-A) "

replace proteinname="Vascular endothelial growth factor D (VEGF-D)" if proteinname=="Vascular endothelial growth factor D (VEGF-D) "

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Till forestplot IMTCCA.dta", replace //IMPROVE data korrigerade för hand

ren proteinname variable

ren beta1 beta

ren se1 se

keep variable beta se study

save, replace

library("metafor")

library("haven")

d2 <- read\_dta("/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Till forestplot IMTCCA.dta")

vars <- unique(d2$variable)

labs <- c("MMP-12", "HGF", "NT-pro-BNP")

par(mfrow = c(2, 2))

for (i in 1:length(labs)) {

inds <- which(grepl(labs[i], d2$variable))

ds <- as.data.frame(d2[inds,])

## I rma och forest finns många options. Kolla i hjälpfilen och ändra efter smak

f <- rma(yi = ds$beta, sei = ds$se, method = "FE")

forest(f, pch = 16, psize = 1.25,

slab = ds$study,

mlab = "Summary",

xlab = "Estimate")

text(0, length(ds$study) + 2, labs[i], font = 2,

cex = 1.3)

}

\*\*\*bulb

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTbulb\_PIVUS.dta"

append using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTBulb\_IMPROVE\_utan log.dta"

append using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTbulb\_MDC.dta"

sort proteinname

replace proteinname="C-C motif chemokine 4 (CCL4)" if proteinname=="C-C motif chemokine 4 (CCL4) "

replace proteinname="CD40 ligand (CD40L)" if proteinname=="CD40 ligand (CD40L) "

replace proteinname="CD40L receptor (CD40)" if proteinname=="CD40L receptor (CD40) "

replace proteinname="Cathepsin D (CTSD)" if proteinname=="Cathepsin D (CTSD) "

replace proteinname="Cystatin-B (CSTB)" if proteinname=="Cystatin-B (CSTB) "

replace proteinname="E-selectin (SELE)" if proteinname=="E-selectin (SELE) "

replace proteinname="Interleukin-8 (IL-8)" if proteinname=="Interleukin-8 (IL-8) "

replace proteinname="Lectin-like oxidized LDL receptor 1 (LOX-1)" if proteinname=="Lectin-like oxidized LDL receptor 1 (LOX-1) "

replace proteinname="Membrane-bound aminopeptidase P (mAmP)" if proteinname=="Membrane-bound aminopeptidase P (mAmP) "

replace proteinname="Myoglobin (MB)" if proteinname=="Myoglobin (MB) "

replace proteinname="Receptor for advanced glycosylation end products (RAGE)" if proteinname=="Receptor for advanced glycosylation end products (RAGE) "

replace proteinname="Renin (REN)" if proteinname=="Renin (REN) "

replace proteinname="Resistin (RETN)" if proteinname=="Resistin (RETN) "

replace proteinname="Thrombomodulin (TM)" if proteinname=="Thrombomodulin "

replace proteinname="Stem cell factor (SCF)" if proteinname=="Stem cell factor (SCF) "

replace proteinname="T-cell immunoglobulin and mucin domain 1 (TIM-1)" if proteinname=="T-cell immunoglobulin and mucin domain 1 (TIM-1) "

replace proteinname="TNF-related activation-induced cytokine (TRANCE)" if proteinname=="TNF-related activation-induced cytokine (TRANCE) "

replace proteinname="TNF-related apoptosis-inducing ligand (TRAIL)" if proteinname=="TNF-related apoptosis-inducing ligand (TRAIL) "

replace proteinname="TNF-related apoptosis-inducing ligand receptor 2 (TRAIL-R2)" if proteinname=="TNF-related apoptosis-inducing ligand receptor 2 (TRAIL-R2) "

replace proteinname="Tumor necrosis factor ligand superfamily member 14 (TNFSF14)" if proteinname=="Tumor necrosis factor ligand superfamily member 14 (TNFSF14) "

replace proteinname="Urokinase plasminogen activator surface receptor (U-PAR)" if proteinname=="Urokinase plasminogen activator surface receptor (U-PAR) "

replace proteinname="Macrophage colony-stimulating factor 1 (CSF-1)" if proteinname=="Macrophage colony-stimulating factor 1 (CSF-1) "

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Till forestplot IMTbulb.dta", replace

ren proteinname variable

ren beta1 beta

ren se1 se

keep variable beta se study

save, replace

library("metafor")

library("haven")

d2 <- read\_dta("/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Till forestplot IMTbulb.dta")

vars <- unique(d2$variable)

labs <- c("MMP-12", "GDF-15", "OPG", "REN", "GH")

par(mfrow = c(3, 2))

for (i in 1:length(labs)) {

inds <- which(grepl(labs[i], d2$variable))

ds <- as.data.frame(d2[inds,])

## I rma och forest finns många options. Kolla i hjälpfilen och ändra efter smak

f <- rma(yi = ds$beta, sei = ds$se, method = "FE")

forest(f, pch = 16, psize = 1.25,

slab = ds$study,

mlab = "Summary",

xlab = "Estimate")

text(0, length(ds$study) + 2, labs[i], font = 2,

cex = 1.3)

}

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*. Bulb

\*ojusterat

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTbulb\_PIVUS.dta"

append using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTBulb\_IMPROVE\_utan log.dta"

append using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTbulb\_MDC.dta"

sort proteinname

replace proteinname="C-C motif chemokine 4 (CCL4)" if proteinname=="C-C motif chemokine 4 (CCL4) "

replace proteinname="CD40 ligand (CD40L)" if proteinname=="CD40 ligand (CD40L) "

replace proteinname="CD40L receptor (CD40)" if proteinname=="CD40L receptor (CD40) "

replace proteinname="Cathepsin D (CTSD)" if proteinname=="Cathepsin D (CTSD) "

replace proteinname="Cystatin-B (CSTB)" if proteinname=="Cystatin-B (CSTB) "

replace proteinname="E-selectin (SELE)" if proteinname=="E-selectin (SELE) "

replace proteinname="Interleukin-8 (IL-8)" if proteinname=="Interleukin-8 (IL-8) "

replace proteinname="Lectin-like oxidized LDL receptor 1 (LOX-1)" if proteinname=="Lectin-like oxidized LDL receptor 1 (LOX-1) "

replace proteinname="Membrane-bound aminopeptidase P (mAmP)" if proteinname=="Membrane-bound aminopeptidase P (mAmP) "

replace proteinname="Myoglobin (MB)" if proteinname=="Myoglobin (MB) "

replace proteinname="Receptor for advanced glycosylation end products (RAGE)" if proteinname=="Receptor for advanced glycosylation end products (RAGE) "

replace proteinname="Renin (REN)" if proteinname=="Renin (REN) "

replace proteinname="Resistin (RETN)" if proteinname=="Resistin (RETN) "

replace proteinname="Thrombomodulin (TM)" if proteinname=="Thrombomodulin "

replace proteinname="Stem cell factor (SCF)" if proteinname=="Stem cell factor (SCF) "

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replace proteinname="TNF-related activation-induced cytokine (TRANCE)" if proteinname=="TNF-related activation-induced cytokine (TRANCE) "

replace proteinname="TNF-related apoptosis-inducing ligand (TRAIL)" if proteinname=="TNF-related apoptosis-inducing ligand (TRAIL) "

replace proteinname="TNF-related apoptosis-inducing ligand receptor 2 (TRAIL-R2)" if proteinname=="TNF-related apoptosis-inducing ligand receptor 2 (TRAIL-R2) "

replace proteinname="Tumor necrosis factor ligand superfamily member 14 (TNFSF14)" if proteinname=="Tumor necrosis factor ligand superfamily member 14 (TNFSF14) "

replace proteinname="Urokinase plasminogen activator surface receptor (U-PAR)" if proteinname=="Urokinase plasminogen activator surface receptor (U-PAR) "

replace proteinname="Macrophage colony-stimulating factor 1 (CSF-1)" if proteinname=="Macrophage colony-stimulating factor 1 (CSF-1) "

ren pvalue1 p

ren proteinname met

ren se1 se

ren beta1 beta

levelsof met, local(levels)

foreach l of local levels {

di "`l'"

}

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

file open a using "metaresultat\_IMTbulb\_unadj\_medMDC\_utan log.txt", replace write

file write a "met" \_tab "beta" \_tab "se" \_tab "p" \_tab "I\_sq" \_n

foreach l of local levels {

metan beta se if met=="`l'", nograph fixedi

file write a "`l'" \_tab (r(ES)) \_tab (r(seES)) \_tab (2\*normal(-abs((r(ES))/(r(seES))))) \_tab (r(i\_sq)) \_n

}

file close a

clear

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

insheet using "metaresultat\_IMTbulb\_unadj\_medMDC\_utan log.txt"

ren met protein

ren beta beta1

ren se se1

ren p p1

ren i\_sq i\_sq1

sort protein

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/metaresultat\_IMTbulb\_unadj\_medMDC\_utan log.dta", replace

\*adjusted

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTbulb\_PIVUS.dta"

append using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTBulb\_IMPROVE\_utan log.dta"

append using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table proteomics vs IMTbulb\_MDC.dta"

sort proteinname

replace proteinname="C-C motif chemokine 4 (CCL4)" if proteinname=="C-C motif chemokine 4 (CCL4) "

replace proteinname="CD40 ligand (CD40L)" if proteinname=="CD40 ligand (CD40L) "

replace proteinname="CD40L receptor (CD40)" if proteinname=="CD40L receptor (CD40) "

replace proteinname="Cathepsin D (CTSD)" if proteinname=="Cathepsin D (CTSD) "

replace proteinname="Cystatin-B (CSTB)" if proteinname=="Cystatin-B (CSTB) "

replace proteinname="E-selectin (SELE)" if proteinname=="E-selectin (SELE) "

replace proteinname="Interleukin-8 (IL-8)" if proteinname=="Interleukin-8 (IL-8) "

replace proteinname="Lectin-like oxidized LDL receptor 1 (LOX-1)" if proteinname=="Lectin-like oxidized LDL receptor 1 (LOX-1) "

replace proteinname="Membrane-bound aminopeptidase P (mAmP)" if proteinname=="Membrane-bound aminopeptidase P (mAmP) "

replace proteinname="Myoglobin (MB)" if proteinname=="Myoglobin (MB) "

replace proteinname="Receptor for advanced glycosylation end products (RAGE)" if proteinname=="Receptor for advanced glycosylation end products (RAGE) "

replace proteinname="Renin (REN)" if proteinname=="Renin (REN) "

replace proteinname="Resistin (RETN)" if proteinname=="Resistin (RETN) "

replace proteinname="Thrombomodulin (TM)" if proteinname=="Thrombomodulin "

replace proteinname="Stem cell factor (SCF)" if proteinname=="Stem cell factor (SCF) "

replace proteinname="T-cell immunoglobulin and mucin domain 1 (TIM-1)" if proteinname=="T-cell immunoglobulin and mucin domain 1 (TIM-1) "

replace proteinname="TNF-related activation-induced cytokine (TRANCE)" if proteinname=="TNF-related activation-induced cytokine (TRANCE) "

replace proteinname="TNF-related apoptosis-inducing ligand (TRAIL)" if proteinname=="TNF-related apoptosis-inducing ligand (TRAIL) "

replace proteinname="TNF-related apoptosis-inducing ligand receptor 2 (TRAIL-R2)" if proteinname=="TNF-related apoptosis-inducing ligand receptor 2 (TRAIL-R2) "

replace proteinname="Tumor necrosis factor ligand superfamily member 14 (TNFSF14)" if proteinname=="Tumor necrosis factor ligand superfamily member 14 (TNFSF14) "

replace proteinname="Urokinase plasminogen activator surface receptor (U-PAR)" if proteinname=="Urokinase plasminogen activator surface receptor (U-PAR) "

replace proteinname="Macrophage colony-stimulating factor 1 (CSF-1)" if proteinname=="Macrophage colony-stimulating factor 1 (CSF-1) "

ren pvalue2 p

ren proteinname met

ren se2 se

ren beta2 beta

levelsof met, local(levels)

foreach l of local levels {

di "`l'"

}

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

file open a using "metaresultat\_IMTbulb\_adj\_medMDC\_utan log.txt", replace write

file write a "met" \_tab "beta" \_tab "se" \_tab "p" \_tab "I\_sq" \_n

foreach l of local levels {

metan beta se if met=="`l'", nograph fixedi

file write a "`l'" \_tab (r(ES)) \_tab (r(seES)) \_tab (2\*normal(-abs((r(ES))/(r(seES))))) \_tab (r(i\_sq)) \_n

}

file close a

clear

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

insheet using "metaresultat\_IMTbulb\_adj\_medMDC\_utan log.txt"

ren met protein

ren beta beta2

ren se se2

ren p p2

ren i\_sq i\_sq2

sort protein

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/metaresultat\_IMTbulb\_adj\_medMDC\_utan log.dta"

\*slå ihop till en tabell

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/metaresultat\_IMTbulb\_unadj\_medMDC\_utan log.dta", clear

merge protein using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/metaresultat\_IMTbulb\_adj\_medMDC\_utan log.dta"

tab \_merge

drop if \_merge!=3

drop \_merge

drop if protein=="Zscore: 169\_ITGB1BP2"

drop if protein=="Zscore: 172\_SIRT2"

drop if protein=="Zscore: 192\_NEMO"

drop if protein=="Protein S100-A12 (EN-RAGE)"

drop if protein=="Beta-nerve growth factor (Beta-NGF)"

drop if protein=="NF-kappa-B essential modulator (NEMO)"

drop if protein=="Natriuretic peptides B (BNP)"

drop if protein=="Agouti-related protein (AGRP)"

drop if protein=="Ovarian cancer-related tumor marker CA 125 (CA-125)"

drop if protein=="SIR2-like protein (SIRT2)"

gen cilower1=beta1-(1.96\*se1)

gen cihigher1=beta1+(1.96\*se1)

gen cilower2=beta2-(1.96\*se2)

gen cihigher2=beta2+(1.96\*se2)

sort p1

drop i\_sq1 i\_sq2

order protein beta1 cilower1 cihigher1 p1 beta2 cilower2 cihigher2 p2

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/metaresultat\_IMTbulb\_medMDC\_till fig\_utan log.dta", replace

\*jämföra CCA-bulb resultat

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/metaresultat\_IMTbulb\_medMDC\_till fig\_utan log.dta"

sort protein

ren p1 p1bulb

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/metaresultat\_IMTbulb\_medMDC\_till fig\_utan log\_p1bulb.dta"

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/metaresultat\_IMTCCA\_medMDC\_till fig\_utan log.dta"

sort protein

merge protein using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/metaresultat\_IMTbulb\_medMDC\_till fig\_utan log\_p1bulb.dta"

tab \_merge

drop \_merge

keep protein p1 p1bulb

sort p1

\*###### catepillarplot CCA

library("haven")

d\_CCA <- read\_dta("/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/metaresultat\_IMTCCA\_medMDC\_till fig\_utan log.dta")

d\_CCA <- d\_CCA[order(d\_CCA$beta2),]

xlims <- c(min(d\_CCA$cilower2) - 0.01, max(d\_CCA$cihigher2) + 0.01)

ylims <- c(-0.02, nrow(d\_CCA) + 1) ## Måste sätta denna annars blir det fel

ycex <- 0.6 ## Storlek på y-labels

library(lattice)

plot\_CCA <- with(d\_CCA,

xyplot(1:nrow(d\_CCA) ~ beta2, data = d\_CCA, xlim = xlims, ylim = ylims,

panel = function(x, y, ...) {

panel.abline(v = 0, lty = 2)

panel.arrows(x0 = cilower2,

y0 = y,

x1 = cihigher2,

y1 = y,

code = 3, length = 0.02,

angle = 90)

panel.xyplot(x, y, pch = 16, col = "black")

}, scales = list(y = list(at = 1:nrow(d\_CCA), lab = protein,

cex = ycex, tck = c(1, 0))),

ylab = "", xlab = expression(beta), main = "IMT - CCA")

)

print(plot\_CCA) # Ändra height till 800 i TIFF

\*###### catepillarplot bulb

library("haven")

d\_bulb <- read\_dta("/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/metaresultat\_IMTbulb\_medMDC\_till fig\_utan log.dta")

d\_bulb <- d\_bulb[order(d\_bulb$beta2),]

xlims <- c(min(d\_bulb$cilower2) - 0.01, max(d\_bulb$cihigher2) + 0.01)

ylims <- c(-0.02, nrow(d\_bulb) + 1) ## Måste sätta denna annars blir det fel

ycex <- 0.6 ## Storlek på y-labels

library(lattice)

plot\_bulb <- with(d\_bulb,

xyplot(1:nrow(d\_bulb) ~ beta2, data = d\_bulb, xlim = xlims, ylim = ylims,

panel = function(x, y, ...) {

panel.abline(v = 0, lty = 2)

panel.arrows(x0 = cilower2,

y0 = y,

x1 = cihigher2,

y1 = y,

code = 3, length = 0.02,

angle = 90)

panel.xyplot(x, y, pch = 16, col = "black")

}, scales = list(y = list(at = 1:nrow(d\_bulb), lab = protein,

cex = ycex, tck = c(1, 0))),

ylab = "", xlab = expression(beta), main = "IMT - bulb")

)

print(plot\_bulb) # Ändra height till 800 i TIFF

\*################ plot IMT CCA vs bulb

library("haven")

d\_imt <- read\_dta("/Users/larslind/Lind kopior/PIVUS pek tander vs athero/PIVUS pek tander vs athero6.dta")

library(rms)

dd <- datadist(d\_imt); options(datadist = "dd")

imt\_spline <- ols(imtfmeansindx2 ~ rcs(bulbimtfmeandxsin, 3) , data = d\_imt)

pred <- Predict(imt\_spline, bulbimtfmeandxsin) ## 200 värden på wt allt annat hållet konstant

plot(Predict(imt\_spline, bulbimtfmeandxsin), adj.subtitle = FALSE, xlab = "IMT-Bulb (mm)", ylab ="IMT-CCA (mm)")

\*############## Densityplot IMT CCA vs bulb

library(reshape)

d\_imt <- rename(d\_imt, c(imtfmeansindx2="IMT\_CCA"))

d\_imt <- rename(d\_imt, c(bulbimtfmeandxsin="IMT\_Bulb"))

bwtheme <- standard.theme("pdf", color=FALSE)

densityplot(~IMT\_CCA + IMT\_Bulb, data = d\_imt, plot.points = FALSE, xlab = "",

par.settings=bwtheme, auto.key = list(space = "top"))

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* Meta-analys av riskfactors for CCA vs Bulb

clear

cd "/Users/larslind/"

use "Lind kopior/Proteomics/PIVUS data proteomics70\_korr.dta"

sort lpnr

merge lpnr using "Lind kopior/PIVUS pek tander vs athero/PIVUS pek tander vs athero6.dta"

sum \_merge

drop \_merge

egen area=rowtotal(areadx areasin), missing

gen lnarea=log(area)

gen lnimtcca=log(imtfmeansindx2)

gen lnimtbulb=log(bulbimtfmeandxsin)

egen plaquegsm=rowmean(areadx areasin)

\*CCA

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

file open table2 using "Table risk factors vs IMTCCA\_PIVUS.txt", replace write

file write table2 "Variable" \_tab "n" \_tab "Beta" \_tab "SE" \_tab "CIlow" \_tab "CIhigh" \_tab "P-value" \_n

foreach var of varlist manuelltsbp hdl ldl bmi diabetesmellitus rkarenu {

quietly: reg lnimtcca `var' kn lpnr

file write table2 "`var'" \_tab (e(N)) \_tab %5.3f (\_b[`var']) \_tab %5.3f (\_se[`var']) \_tab %5.3f (\_b[`var']-1.96\*\_se[`var']) \_tab %5.3f (\_b[`var']+1.96\*\_se[`var']) \_tab %12.10f (round(2\*(ttail(e(df\_r),abs(\_b[`var']/\_se[`var']))),0.000000000000001)) \_n

}

file close table2

\*Bulb

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

file open table2 using "Table risk factors vs IMTbulb\_PIVUS.txt", replace write

file write table2 "Variable" \_tab "n" \_tab "Beta" \_tab "SE" \_tab "CIlow" \_tab "CIhigh" \_tab "P-value" \_n

foreach var of varlist manuelltsbp hdl ldl bmi diabetesmellitus rkarenu {

quietly: reg lnimtbulb `var' kn lpnr

file write table2 "`var'" \_tab (e(N)) \_tab %5.3f (\_b[`var']) \_tab %5.3f (\_se[`var']) \_tab %5.3f (\_b[`var']-1.96\*\_se[`var']) \_tab %5.3f (\_b[`var']+1.96\*\_se[`var']) \_tab %12.10f (round(2\*(ttail(e(df\_r),abs(\_b[`var']/\_se[`var']))),0.000000000000001)) \_n

}

file close table2

\*preparera inför meta-analysen

\*MDC

clear

import delimited "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Risk factors\_CCA\_MDC.txt", encoding(ISO-8859-1)

replace riskfactor="SBP" if riskfactor=="systolic blood pressure"

gen study="MDC"

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Risk factors\_CCA\_MDC.dta", replace

clear

import delimited "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Risk factors\_Bulb\_MDC.txt", encoding(ISO-8859-1)

replace riskfactor="SBP" if riskfactor=="systolic blood pressure"

gen study="MDC"

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Risk factors\_Bulb\_MDC.dta", replace

\*PIVUS

clear

import delimited "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table risk factors vs IMTbulb\_PIVUS.txt", encoding(ISO-8859-1)

ren variable riskfactor

replace riskfactor="SBP" if riskfactor=="manuelltsbp"

replace riskfactor="HDL" if riskfactor=="hdl"

replace riskfactor="LDL" if riskfactor=="ldl"

replace riskfactor="BMI" if riskfactor=="bmi"

replace riskfactor="Diabetes" if riskfactor=="diabetesmellitus"

replace riskfactor="Smoking" if riskfactor=="rkarenu"

gen study="PIVUS"

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Risk factors\_Bulb\_PIVUS.dta"

clear

import delimited "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Table risk factors vs IMTCCA\_PIVUS.txt", encoding(ISO-8859-1)

ren variable riskfactor

replace riskfactor="SBP" if riskfactor=="manuelltsbp"

replace riskfactor="HDL" if riskfactor=="hdl"

replace riskfactor="LDL" if riskfactor=="ldl"

replace riskfactor="BMI" if riskfactor=="bmi"

replace riskfactor="Diabetes" if riskfactor=="diabetesmellitus"

replace riskfactor="Smoking" if riskfactor=="rkarenu"

gen study="PIVUS"

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Risk factors\_CCA\_PIVUS.dta"

\*IMPROVE

clear

import delimited "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Risk factors\_CCA\_IMPROVE.txt", encoding(ISO-8859-1)

replace riskfactor="SBP" if riskfactor=="systolic blood pressure"

gen study="IMPROVE"

replace cilow = ".0005588" in 4

destring cilow, replace

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Risk factors\_CCA\_IMPROVE.dta", replace

clear

import delimited "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Risk factors\_Bulb\_IMPROVE.txt", encoding(ISO-8859-1)

replace riskfactor="SBP" if riskfactor=="systolic blood pressure"

gen study="IMPROVE"

replace cilow = "-.0018129" in 4

replace cihigh = .002979 in 4

destring cilow, replace

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Risk factors\_Bulb\_IMPROVE.dta", replace

\*Själva meta-analysen

\*CCA

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Risk factors\_CCA\_MDC.dta"

append using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Risk factors\_CCA\_PIVUS.dta"

append using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Risk factors\_CCA\_IMPROVE.dta"

ren pvalue p

ren riskfactor met

ren se se

ren beta beta

levelsof met, local(levels)

foreach l of local levels {

di "`l'"

}

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

file open a using "metaresultat\_risk factors vs CCA.txt", replace write

file write a "met" \_tab "beta" \_tab "se" \_tab "p" \_tab "I\_sq" \_n

foreach l of local levels {

metan beta se if met=="`l'", nograph fixedi

file write a "`l'" \_tab (r(ES)) \_tab (r(seES)) \_tab (2\*normal(-abs((r(ES))/(r(seES))))) \_tab (r(i\_sq)) \_n

}

file close a

clear

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

insheet using "metaresultat\_risk factors vs CCA.txt"

ren met riskfactor

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/metaresultat\_risk factors vs CCA.dta", replace

\*bulb

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Risk factors\_Bulb\_MDC.dta"

append using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Risk factors\_Bulb\_PIVUS.dta"

append using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Risk factors\_Bulb\_IMPROVE.dta"

ren pvalue p

ren riskfactor met

ren se se

ren beta beta

levelsof met, local(levels)

foreach l of local levels {

di "`l'"

}

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

file open a using "metaresultat\_risk factors vs Bulb.txt", replace write

file write a "met" \_tab "beta" \_tab "se" \_tab "p" \_tab "I\_sq" \_n

foreach l of local levels {

metan beta se if met=="`l'", nograph fixedi

file write a "`l'" \_tab (r(ES)) \_tab (r(seES)) \_tab (2\*normal(-abs((r(ES))/(r(seES))))) \_tab (r(i\_sq)) \_n

}

file close a

clear

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

insheet using "metaresultat\_risk factors vs Bulb.txt"

ren met riskfactor

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/metaresultat\_risk factors vs Bulb.dta", replace

\*beräkning av p-värde

dis (2\*normal(-abs(.0116803/.000293)))

xxxxx

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*. Beräkning till manus om skillnad IMTCCA vs IMTbulb avseende allstrokeMI - Bootstrap

clear

cd "/Users/larslind/"

use "Lind kopior/PIVUS pek tander vs athero/PIVUS pek tander vs athero6.dta"

sort lpnr

merge lpnr using "Lind kopior/PIVUS data 70-75-CF/PIVUS75 data-CF/PIVUS75 data basalfil.dta"

sum \_merge

drop \_merge

sort lpnr

merge lpnr using "Lind kopior/PIVUS data 70-75-CF/PIVUS80 data-CF/PIVUS80 data CVoutcomes\_CF.dta"

sum \_merge

drop \_merge

sort lpnr

merge lpnr using "Lind kopior/PIVUS data 70-75-CF/PIVUS75 data-CF/PIVUS75 data IMT.dta"

sum \_merge

drop \_merge

sort lpnr

merge lpnr using "Lind kopior/PIVUS data 70-75-CF/PIVUS75 data-CF/PIVUs75 data carotisplaque.dta"

sum \_merge

drop \_merge

sort lpnr

merge lpnr using "Lind kopior/PIVUS data adjusted IM-GSM.dta"

sum \_merge

drop \_merge

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*generera AllMI

gen allmi=.

replace allmi=0 if mi!=.

replace allmi=1 if mi==1 & mi!=.

replace allmi=1 if CVtypedead=="mi"

tab allmi

gen allmidatestata= exitdatestata

replace allmidatestata = midatestata if midatestata<exitdatestata

format allmidatestata %d

\*drop if validmi70==1 // for longitudinal analysis

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*generera AllStroke

gen allstroke=.

replace allstroke =0 if stroke!=.

replace allstroke =1 if stroke ==1 & stroke!=.

replace allstroke =1 if CVtypedead=="stroke\_inf"

replace allstroke =1 if CVtypedead=="stroke\_blod"

tab allstroke

gen allstrokedatestata= exitdatestata

replace allstrokedatestata = strokedatestata if strokedatestata <exitdatestata

format allstrokedatestata %d

\*drop if validstroke70==1

\*drop if tiastroke==1 // om man inte vill ha med TIA

\*drop if blodningstroke ==1 // om man inte vill ha med blödningarna

\*\*\*\*\*\*\*\*\*\*generera allsvikt

gen allsvikt=.

replace allsvikt =0 if svikt!=.

replace allsvikt =1 if svikt ==1 & svikt!=.

replace allsvikt =1 if CVtypedead=="svikt"

tab allsvikt

gen allsviktdatestata= exitdatestata

replace allsviktdatestata = sviktdatestata if sviktdatestata <exitdatestata

format allsviktdatestata %d

\*drop if hjrtsvikt ==1

\*\*\*\*\*\*\*generera allCVD

gen allCVD=allmi if allmi!=.

replace allCVD=1 if allstroke==1 & allstroke!=.

replace allCVD=1 if allsvikt==1 & allsvikt!=.

tab allCVD

gen allCVDdatestata= allmidatestata

replace allCVDdatestata = allstrokedatestata if allstrokedatestata <allCVDdatestata

replace allCVDdatestata = allsviktdatestata if allsviktdatestata <allCVDdatestata

format allCVDdatestata %d

tab allCVD

tab allCVD if validmi70==0 & validstroke70==0 & hjrtsvikt ==0 & tiastroke==0

\*\*\*\*\*\*\*generera allMIStoke

gen allMIStroke =allmi if allmi!=.

replace allMIStroke =1 if allstroke==1 & allstroke!=.

tab allMIStroke

gen allMIStrokedatestata= allmidatestata

replace allMIStrokedatestata = allstrokedatestata if allstrokedatestata <allMIStrokedatestata

format allMIStrokedatestata %d

tab allMIStroke if validmi70==0 & validstroke70==0 & tiastroke==0

drop if validstroke70==1

drop if validmi70==1

drop if tiastroke==1

drop if allMIStrokedatestata<beskdat70mdy

tab allMIStroke

ren imtfmeansindx2 imtCCA70

ren bulbimtfmeandxsin imtBULB70

ren gsmimtdxsin imGSM70

ren imtfmeandxsin75 imtCCA75

ren bilbimtsindx75 imtBULB75

ren ccaimgsm75 imGSM75

replace areadx75=0 if areadx75==.

replace areasin75=0 if areasin75==.

gen area75=areadx75 +areasin75

replace area75=. if imtCCA75==.

sum area75

tab area75

gen anyplaque10at75=.

replace anyplaque10at75=0 if area75!=.

replace anyplaque10at75=1 if area75!=. & area75>10

tab anyplaque10at75

replace areadx=0 if areadx==.

replace areasin=0 if areasin==.

gen area=areadx +areasin

replace area=. if imtCCA70 ==.

gen anyplaque10=.

replace anyplaque10=0 if area!=.

replace anyplaque10=1 if area!=. & area>10

ren anyplaque10 anyplaque10at70

tab anyplaque10at70

ren area area70

ren nrofarterieswithplaque nrofarterieswithplaque70

ren plaquegsmsin75 plaqueGSM75

ren worstgsmplaque plaqueGSM70

ren beskdat70mdy date70

ren beskdat75mdy date75

ren bmi bmi70

ren manuelltsbp manuelltsbp70

ren medicinmothgtbt medicinmothgtbt70

ren statiner statiner70

ren rkarenu rkarenu70

ren hdl hdl70

ren ldl ldl70

ren diabetesmellitus diabetesmellitus70

ren diabetesmell75 diabetesmellitus75

ren mage mage70

gen kvadadjustedimgsm70= adjustedimgsm70\* adjustedimgsm70

gen kvadadjustedimgsm75= adjustedimgsm75\* adjustedimgsm75

keep lpnr anyplaque10at70 anyplaque10at75 area70 area75 adjustedimgsm70 adjustedimgsm75 kvadadjustedimgsm70 kvadadjustedimgsm75 imtCCA70 imtCCA75 imtBULB70 imtBULB75 imGSM70 imGSM75 nrofarterieswithplaque70 nrofarterieswithplaque75 plaqueGSM70 plaqueGSM75 utbildning13 mage70 mage75 diabetesmellitus70 diabetesmellitus75 hdl70 hdl75 ldl70 ldl75 rkarenu70 rkarenu75 bmi70 bmi75 manuelltsbp70 manuelltsbp75 medicinmothgtbt70 medicinmothgtbt75 statiner70 statiner75 kn date70 date75 birthdate dead exitdatestata allCVD allCVDdatestata allMIStrokedatestata allMIStroke

\*reshapa datasetet

reshape long anyplaque10at area adjustedimgsm kvadadjustedimgsm imtCCA imtBULB imGSM nrofarterieswithplaque plaqueGSM mage bmi manuelltsbp medicinmothgtbt statiner rkarenu hdl ldl diabetesmellitus date, i(lpnr) j(visit)

drop if date==.

\*fixa med datumen vs all CVD

gen last=1 if lpnr!=lpnr[\_n+1]

expand 2 if last==1

sort lpnr date

replace date= allMIStrokedatestata if last==1 & last[\_n-1]==1 & lpnr==lpnr[\_n-1] // sätt in exitdatum för rätt outcome här \*\*\*\*\*\* MI+Stroke

gen status=0

replace status=1 if allMIStroke==1 & last==1 & last[\_n-1]==1 & lpnr==lpnr[\_n-1] // sätt in rätt outcome här

snapspan lpnr date status, replace gen(time0)

drop if time0==.

\*MI+Stroke

stset date, fail(status) enter(time0) id(lpnr) origin(birthdate) scale(365.25) // ändra ej exitdatum eller ngt annat här

stdes

stcox imtCCA kn bmi manuelltsbp medicinmothgtbt statiner rkarenu hdl ldl diabetesmellitus if imtCCA!=. & imtBULB!=.

stcox imtBULB kn bmi manuelltsbp medicinmothgtbt statiner rkarenu hdl ldl diabetesmellitus if imtCCA!=. & imtBULB!=.

\*på sd skala

gen lnimtCCA=log(imtCCA)

gen lnimtBULB=log(imtBULB)

egen stdimtCCA=std(lnimtCCA)

egen stdimtBULB=std(lnimtBULB)

stcox stdimtCCA kn if imtCCA!=. & imtBULB!=.

stcox stdimtCCA kn bmi manuelltsbp medicinmothgtbt statiner rkarenu hdl ldl diabetesmellitus if imtCCA!=. & imtBULB!=.

stcox stdimtBULB kn if imtCCA!=. & imtBULB!=.

stcox stdimtBULB kn bmi manuelltsbp medicinmothgtbt statiner rkarenu hdl ldl diabetesmellitus if imtCCA!=. & imtBULB!=.

\* bootstrap for difference between two coefficients

\* make your bootstrap program

cap program drop myboot

program myboot, rclass

stcox stdimtCCA kn bmi manuelltsbp medicinmothgtbt statiner rkarenu hdl ldl diabetesmellitus if imtCCA!=. & imtBULB!=.

return scalar coef1=exp(\_b[stdimtCCA])

stcox stdimtBULB kn bmi manuelltsbp medicinmothgtbt statiner rkarenu hdl ldl diabetesmellitus if imtCCA!=. & imtBULB!=.

return scalar coef2=exp(\_b[stdimtBULB])

end

\* run your program

myboot

ret list

bootstrap "myboot" coef1=r(coef1) coef2=r(coef2), reps(10000) saving("/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/bootstrapsample") replace

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/bootstrapsample",clear

sum coef1 coef2

\* differences between coefficients and 95% CIs

gen coefdiff12 = coef1-coef2

label var coefdiff12 "Difference between 1 & 2"

sum coefdiff12

centile coefdiff12, c(2.5,97.5)

cap program drop myboot

program myboot, rclass

stcox imtCCA kn bmi manuelltsbp medicinmothgtbt statiner rkarenu hdl ldl diabetesmellitus if imtCCA!=. & imtBULB!=., nohr

return scalar coef1=\_b[imtCCA]

stcox imtBULB kn bmi manuelltsbp medicinmothgtbt statiner rkarenu hdl ldl diabetesmellitus if imtCCA!=. & imtBULB!=., nohr

return scalar coef2=\_b[imtBULB]

end

\* run your program

myboot

ret list

bootstrap "myboot" coef1=r(coef1) coef2=r(coef2), reps(100) saving("/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/bootstrapsample") replace

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/bootstrapsample",clear

sum coef1 coef2

\* differences between coefficients and 95% CIs

gen coefdiff12 = coef1-coef2

label var coefdiff12 "Difference between 1 & 2"

sum coefdiff12

centile coefdiff12, c(2.5,97.5)

clear

set obs 64

g n=int(uniform()\*10)

g x=1+int((\_n-1)/8)

g y=1+mod((\_n-1),8)

la def xlab 1 "one" 2 "two" 7 "seven" 8 "eight"

la def ylab 3 "three" 4 "four" 5 "five" 6 "six"

la val x xlab

la val y ylab

ta y x [fw=n]

hmap x y n,mono

hmap x y n, sc

\*\*\*\*\*\*\*\*\* SEM analys

ren visit time

sort lpnr time

merge lpnr time using "/Users/larslind/Lind kopior/PIVUS data/Long format/PIVUS data 70\_75 proteomics\_long.dta"

tab \_merge

drop \_merge

sem (imtBULB -> allMIStroke, ) (MMP\_12 -> allMIStroke, ) (kn -> MMP\_12, ) ///

(kn -> imtBULB,) (kn -> allMIStroke, ) (imtBULB -> MMP\_12, ), method(mlmv) nocapslatent

estat teffects

sem (imtBULB -> allMIStroke, ) (GDF\_15 -> allMIStroke, ) (kn -> GDF\_15, ) ///

(kn -> imtBULB,) (kn -> allMIStroke, ) (imtBULB -> GDF\_15, ), method(mlmv) nocapslatent

estat teffects

sem (imtBULB -> allMIStroke, ) (MMP\_12 -> allMIStroke, ) (kn -> MMP\_12, ) ///

(kn -> imtBULB,) (kn -> allMIStroke, ) (MMP\_12 -> imtBULB , ), method(mlmv) nocapslatent

estat teffects

sem (imtBULB -> allMIStroke, ) (GDF\_15 -> allMIStroke, ) (kn -> GDF\_15, ) ///

(kn -> imtBULB,) (kn -> allMIStroke, ) (GDF\_15 -> imtBULB, ), method(mlmv) nocapslatent

estat teffects

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* Proteiner vs atherooutcomes

clear

cd "/Users/larslind/"

use "Lind kopior/PIVUS pek tander vs athero/PIVUS pek tander vs athero6.dta"

sort lpnr

merge lpnr using "Lind kopior/Proteomics/PIVUS data proteomics70\_korr.dta"

sum \_merge

drop \_merge

sort lpnr

merge lpnr using "/Users/larslind/Lind kopior/PIVUS data/Outcomes/PIVUS85 outcomes.dta"

sum \_merge

drop \_merge

\*proteiner redan på SD-skala, annars transformera dem!

\*\*\*\*\*\*\*\* combined endpoint, MI+ischemic stroke

drop if prevalentmi70==1

drop if prevalentstroke70==1

stset allatherodate15y, fail(allathero15y) id(lpnr) enter(birthdate) origin(beskdat70mdy) scale(365.25) // 147 cases, PYAR 11928, medain follow-up 15.0, range 0.18- 15.9

stdes

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

file open table2 using "Regression table\_proteomics vs atherooutcome.txt", replace write

\*file write table2 \_tab "Gender adjusted" \_tab \_tab "Multiple adjusted" \_n

file write table2 "Variable" \_tab "n1" \_tab "beta1" \_tab "SE1" \_tab "P-value1" \_tab \_tab "n2" \_tab "beta2" \_tab "SE2" \_tab "P-value2" \_n

\*lägg till age i modellen om det behövs

foreach var of varlist prot\* {

quietly:stcox `var' kn, nohr

file write table2 "`var'" \_tab (e(N)) \_tab (round(\_b[`var'],0.00001)) \_tab (round(\_se[`var'],0.00001)) \_tab (round(2\*(1-normal(abs(\_b[`var']/\_se[`var']))),0.00000001)) \_tab

quietly:stcox `var' kn rkarenu hdl ldl bmi diabetesmellitus manuelltsbp, nohr

file write table2 \_tab (e(N)) \_tab (round(\_b[`var'],0.00001)) \_tab (round(\_se[`var'],0.00001)) \_tab (round(2\*(1-normal(abs(\_b[`var']/\_se[`var']))),0.00000001)) \_n

}

file close table2

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

insheet using "Regression table\_proteomics vs atherooutcome.txt", clear

sort variable

merge variable using "/Users/larslind//Lind kopior/Proteomics/proteinnamn\_korr.dta" // merga för att få rätt proteinnamn

drop if \_merge!=3

drop \_merge

keep proteinname n1 beta1 se1 pvalue1 n2 beta2 se2 pvalue2

order proteinname n1 beta1 se1 pvalue1 n2 beta2 se2 pvalue2

sort proteinname

outsheet using "Regression table\_proteomics vs atherooutcome\_metaanalys\_PIVUS.txt", replace noquote

save "Regression table\_proteomics vs atherooutcome\_metaanalys\_PIVUS.dta", replace

\*\*\*\*\*\*bara MI

drop if prevalentmi70==1

\*drop if prevalentstroke70==1

stset midate15y, fail(mi15y) id(lpnr) enter(birthdate) origin(beskdat70mdy) scale(365.25) // 84 cases, PYAR 12276, medain follow-up 15.0, range 0.18- 15.9

stdes

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

file open table2 using "Regression table\_proteomics vs MI15y.txt", replace write

\*file write table2 \_tab "Gender adjusted" \_tab \_tab "Multiple adjusted" \_n

file write table2 "Variable" \_tab "n1" \_tab "beta1" \_tab "SE1" \_tab "P-value1" \_tab \_tab "n2" \_tab "beta2" \_tab "SE2" \_tab "P-value2" \_n

\*lägg till age i modellen om det behövs

foreach var of varlist prot\* {

quietly:stcox `var' kn, nohr

file write table2 "`var'" \_tab (r(N)) \_tab (round(\_b[`var'],0.00001)) \_tab (round(\_se[`var'],0.00001)) \_tab (round(2\*(1-normal(abs(\_b[`var']/\_se[`var']))),0.00000001)) \_tab

quietly:stcox `var' kn rkarenu hdl ldl bmi diabetesmellitus manuelltsbp, nohr

file write table2 \_tab (r(N)) \_tab (round(\_b[`var'],0.00001)) \_tab (round(\_se[`var'],0.00001)) \_tab (round(2\*(1-normal(abs(\_b[`var']/\_se[`var']))),0.00000001)) \_n

}

file close table2

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

insheet using "Regression table\_proteomics vs MI15y.txt", clear

sort variable

merge variable using "/Users/larslind//Lind kopior/Proteomics/proteinnamn\_korr.dta" // merga för att få rätt proteinnamn

drop if \_merge!=3

drop \_merge

keep proteinname beta1 se1 pvalue1 beta2 se2 pvalue2

order proteinname beta1 se1 pvalue1 beta2 se2 pvalue2

sort proteinname

outsheet using "Regression table\_proteomics vs MI15y\_metaanalys\_PIVUS.txt", replace noquote

save "Regression table\_proteomics vs MI15y\_metaanalys\_PIVUS.dta", replace

\*\*\*\*\*\* bara stroke

\*drop if prevalentmi70==1

drop if prevalentstroke70==1

stset infarktstrokedate15y, fail(infarktstroke15y) id(lpnr) enter(birthdate) origin(beskdat70mdy) scale(365.25) // 89 cases, PYAR 12588, medain follow-up 15.0, range 0.18- 15.9

stdes

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

file open table2 using "Regression table\_proteomics vs Stroke15y.txt", replace write

\*file write table2 \_tab "Gender adjusted" \_tab \_tab "Multiple adjusted" \_n

file write table2 "Variable" \_tab "n1" \_tab "beta1" \_tab "SE1" \_tab "P-value1" \_tab \_tab "n2" \_tab "beta2" \_tab "SE2" \_tab "P-value2" \_n

\*lägg till age i modellen om det behövs

foreach var of varlist prot\* {

quietly:stcox `var' kn, nohr

file write table2 "`var'" \_tab (r(N)) \_tab (round(\_b[`var'],0.00001)) \_tab (round(\_se[`var'],0.00001)) \_tab (round(2\*(1-normal(abs(\_b[`var']/\_se[`var']))),0.00000001)) \_tab

quietly:stcox `var' kn rkarenu hdl ldl bmi diabetesmellitus manuelltsbp, nohr

file write table2 \_tab (r(N)) \_tab (round(\_b[`var'],0.00001)) \_tab (round(\_se[`var'],0.00001)) \_tab (round(2\*(1-normal(abs(\_b[`var']/\_se[`var']))),0.00000001)) \_n

}

file close table2

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

insheet using "Regression table\_proteomics vs Stroke15y.txt", clear

sort variable

merge variable using "/Users/larslind//Lind kopior/Proteomics/proteinnamn\_korr.dta" // merga för att få rätt proteinnamn

drop if \_merge!=3

drop \_merge

keep proteinname beta1 se1 pvalue1 beta2 se2 pvalue2

order proteinname beta1 se1 pvalue1 beta2 se2 pvalue2

sort proteinname

outsheet using "Regression table\_proteomics vs Stroke15y\_metaanalys\_PIVUS.txt", replace noquote

save "Regression table\_proteomics vs Stroke15y\_metaanalys\_PIVUS.dta", replace

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* Proteiner vs atherooutcomes i PIVUS

clear

cd "/Users/larslind/"

use "Lind kopior/PIVUS pek tander vs athero/PIVUS pek tander vs athero6.dta"

sort lpnr

merge lpnr using "Lind kopior/Proteomics/PIVUS data proteomics70\_korr.dta"

sum \_merge

drop \_merge

sort lpnr

merge lpnr using "/Users/larslind/Lind kopior/PIVUS data/Outcomes/PIVUS85 outcomes.dta"

sum \_merge

drop \_merge

\*proteiner redan på SD-skala, annars transformera dem!

\*\*\*\*\*\*\*\* combined endpoint, MI+ischemic stroke

drop if prevalentmi70==1

drop if prevalentstroke70==1

stset allatherodate15y, fail(allathero15y) id(lpnr) enter(birthdate) origin(beskdat70mdy) scale(365.25) // 147 cases, PYAR 11928, medain follow-up 15.0, range 0.18- 15.9

stdes

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

file open table2 using "Regression table\_proteomics vs atherooutcome.txt", replace write

\*file write table2 \_tab "Gender adjusted" \_tab \_tab "Multiple adjusted" \_n

file write table2 "Variable" \_tab "n1" \_tab "beta1" \_tab "SE1" \_tab "P-value1" \_tab \_tab "n2" \_tab "beta2" \_tab "SE2" \_tab "P-value2" \_n

\*lägg till age i modellen om det behövs

foreach var of varlist prot\* {

quietly:stcox `var' kn, nohr

file write table2 "`var'" \_tab (r(N)) \_tab (round(\_b[`var'],0.00001)) \_tab (round(\_se[`var'],0.00001)) \_tab (round(2\*(1-normal(abs(\_b[`var']/\_se[`var']))),0.00000001)) \_tab

quietly:stcox `var' kn rkarenu hdl ldl bmi diabetesmellitus manuelltsbp, nohr

file write table2 \_tab (r(N)) \_tab (round(\_b[`var'],0.00001)) \_tab (round(\_se[`var'],0.00001)) \_tab (round(2\*(1-normal(abs(\_b[`var']/\_se[`var']))),0.00000001)) \_n

}

file close table2

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

insheet using "Regression table\_proteomics vs atherooutcome.txt", clear

sort variable

merge variable using "/Users/larslind//Lind kopior/Proteomics/proteinnamn\_korr.dta" // merga för att få rätt proteinnamn

drop if \_merge!=3

drop \_merge

gen study="PIVUS"

keep proteinname beta1 se1 pvalue1 beta2 se2 pvalue2 study

order proteinname beta1 se1 pvalue1 beta2 se2 pvalue2 study

sort proteinname

outsheet using "Regression table\_proteomics vs atherooutcome\_metaanalys\_PIVUS.txt", replace noquote

save "Regression table\_proteomics vs atherooutcome\_metaanalys\_PIVUS.dta", replace

\*\*\*\*\*\*bara MI

drop if prevalentmi70==1

\*drop if prevalentstroke70==1

stset midate15y, fail(mi15y) id(lpnr) enter(birthdate) origin(beskdat70mdy) scale(365.25) // 84 cases, PYAR 12276, medain follow-up 15.0, range 0.18- 15.9

stdes

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

file open table2 using "Regression table\_proteomics vs MI15y.txt", replace write

\*file write table2 \_tab "Gender adjusted" \_tab \_tab "Multiple adjusted" \_n

file write table2 "Variable" \_tab "n1" \_tab "beta1" \_tab "SE1" \_tab "P-value1" \_tab \_tab "n2" \_tab "beta2" \_tab "SE2" \_tab "P-value2" \_n

\*lägg till age i modellen om det behövs

foreach var of varlist prot\* {

quietly:stcox `var' kn, nohr

file write table2 "`var'" \_tab (r(N)) \_tab (round(\_b[`var'],0.00001)) \_tab (round(\_se[`var'],0.00001)) \_tab (round(2\*(1-normal(abs(\_b[`var']/\_se[`var']))),0.00000001)) \_tab

quietly:stcox `var' kn rkarenu hdl ldl bmi diabetesmellitus manuelltsbp, nohr

file write table2 \_tab (r(N)) \_tab (round(\_b[`var'],0.00001)) \_tab (round(\_se[`var'],0.00001)) \_tab (round(2\*(1-normal(abs(\_b[`var']/\_se[`var']))),0.00000001)) \_n

}

file close table2

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

insheet using "Regression table\_proteomics vs MI15y.txt", clear

sort variable

merge variable using "/Users/larslind//Lind kopior/Proteomics/proteinnamn\_korr.dta" // merga för att få rätt proteinnamn

drop if \_merge!=3

drop \_merge

gen study="PIVUS"

keep proteinname beta1 se1 pvalue1 beta2 se2 pvalue2 study

order proteinname beta1 se1 pvalue1 beta2 se2 pvalue2 study

sort proteinname

outsheet using "Regression table\_proteomics vs MI15y\_metaanalys\_PIVUS.txt", replace noquote

save "Regression table\_proteomics vs MI15y\_metaanalys\_PIVUS.dta", replace

\*\*\*\*\*\* bara stroke

\*drop if prevalentmi70==1

drop if prevalentstroke70==1

stset infarktstrokedate15y, fail(infarktstroke15y) id(lpnr) enter(birthdate) origin(beskdat70mdy) scale(365.25) // 89 cases, PYAR 12588, medain follow-up 15.0, range 0.18- 15.9

stdes

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

file open table2 using "Regression table\_proteomics vs Stroke15y.txt", replace write

\*file write table2 \_tab "Gender adjusted" \_tab \_tab "Multiple adjusted" \_n

file write table2 "Variable" \_tab "n1" \_tab "beta1" \_tab "SE1" \_tab "P-value1" \_tab \_tab "n2" \_tab "beta2" \_tab "SE2" \_tab "P-value2" \_n

\*lägg till age i modellen om det behövs

foreach var of varlist prot\* {

quietly:stcox `var' kn, nohr

file write table2 "`var'" \_tab (r(N)) \_tab (round(\_b[`var'],0.00001)) \_tab (round(\_se[`var'],0.00001)) \_tab (round(2\*(1-normal(abs(\_b[`var']/\_se[`var']))),0.00000001)) \_tab

quietly:stcox `var' kn rkarenu hdl ldl bmi diabetesmellitus manuelltsbp, nohr

file write table2 \_tab (r(N)) \_tab (round(\_b[`var'],0.00001)) \_tab (round(\_se[`var'],0.00001)) \_tab (round(2\*(1-normal(abs(\_b[`var']/\_se[`var']))),0.00000001)) \_n

}

file close table2

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

insheet using "Regression table\_proteomics vs Stroke15y.txt", clear

sort variable

merge variable using "/Users/larslind//Lind kopior/Proteomics/proteinnamn\_korr.dta" // merga för att få rätt proteinnamn

drop if \_merge!=3

drop \_merge

gen study="PIVUS"

keep proteinname beta1 se1 pvalue1 beta2 se2 pvalue2 study

order proteinname beta1 se1 pvalue1 beta2 se2 pvalue2 study

sort proteinname

outsheet using "Regression table\_proteomics vs Stroke15y\_metaanalys\_PIVUS.txt", replace noquote

save "Regression table\_proteomics vs Stroke15y\_metaanalys\_PIVUS.dta", replace

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* Discovery in MDC

clear

import delimited "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Results\_metaanalysis for proteins vs combined end-point\_MDC.txt"

drop if pvalue==.

sort pvalue

gen radnummer=\_n

gen vv3= 0.05\*(radnummer/86)

gen FDRyes=0

replace FDRyes=1 if pvalue <vv3

keep if FDRyes==1

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/combined outcome\_MDC\_FDRpos.dta", replace

keep protein

sort protein

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/combined outcome\_MDC\_FDRpos\_proteinname.dta", replace

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* Validation

\*SAVA

clear

import delimited "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Results\_metaanalysis for proteins vs combined end-point \_SAVA.txt"

ren beta beta1

ren se se1

ren pvalue pvalue1

ren v10 beta2

ren v11 se2

ren v14 pvalue2

ren protein proteinname

gen study="SAVA"

keep proteinname beta1 se1 pvalue1 beta2 se2 pvalue2 study

order proteinname beta1 se1 pvalue1 beta2 se2 pvalue2 study

save "Regression table\_proteomics vs atherooutcome\_metaanalys\_SAVA.dta", replace

\*CARDIPP

clear

import delimited "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Results\_metaanalysis for proteins vs combined end-point \_CARDIPP.txt"

ren beta beta1

ren se se1

ren pvalue pvalue1

ren v10 beta2

ren v11 se2

ren v14 pvalue2

ren protein proteinname

gen study="CARDIPP"

keep proteinname beta1 se1 pvalue1 beta2 se2 pvalue2 study

order proteinname beta1 se1 pvalue1 beta2 se2 pvalue2 study

save "Regression table\_proteomics vs atherooutcome\_metaanalys\_CARDIPP.dta", replace

\*IMPROVE

clear

import delimited "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/Results\_metaanalysis for proteins vs combinedendpoints\_IMPROVE.txt"

ren beta beta1

ren se se1

ren pvalue pvalue1

ren v10 beta2

ren v11 se2

ren v14 pvalue2

ren protein proteinname

gen study="IMPROVE"

keep proteinname beta1 se1 pvalue1 beta2 se2 pvalue2 study

order proteinname beta1 se1 pvalue1 beta2 se2 pvalue2 study

save "Regression table\_proteomics vs atherooutcome\_metaanalys\_IMPROVE.dta", replace

\*\*\*\*\*\*\*\*\*\*\*\* Metaanalys ojusterat

clear

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

use "Regression table\_proteomics vs atherooutcome\_metaanalys\_CARDIPP.dta"

append using "Regression table\_proteomics vs atherooutcome\_metaanalys\_SAVA.dta"

append using "Regression table\_proteomics vs atherooutcome\_metaanalys\_PIVUS.dta"

append using "Regression table\_proteomics vs atherooutcome\_metaanalys\_IMPROVE.dta"

sort proteinname

ren pvalue1 p

ren proteinname met

ren se1 se

ren beta1 beta

levelsof met, local(levels)

foreach l of local levels {

di "`l'"

}

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

file open a using "metaresultat\_atherooutcome\_unadj.txt", replace write

file write a "met" \_tab "beta" \_tab "se" \_tab "p" \_tab "I\_sq" \_n

foreach l of local levels {

metan beta se if met=="`l'", nograph fixedi

file write a "`l'" \_tab (r(ES)) \_tab (r(seES)) \_tab (2\*normal(-abs((r(ES))/(r(seES))))) \_tab (r(i\_sq)) \_n

}

file close a

clear

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

insheet using "metaresultat\_atherooutcome\_unadj.txt"

ren met protein

ren beta beta1

ren se se1

ren p p1

ren i\_sq i\_sq1

sort protein

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/metaresultat\_atherooutcome\_unadj.dta", replace

\*adjusted

clear

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

use "Regression table\_proteomics vs atherooutcome\_metaanalys\_CARDIPP.dta"

append using "Regression table\_proteomics vs atherooutcome\_metaanalys\_SAVA.dta"

append using "Regression table\_proteomics vs atherooutcome\_metaanalys\_PIVUS.dta"

append using "Regression table\_proteomics vs atherooutcome\_metaanalys\_IMPROVE.dta"

sort proteinname

ren pvalue2 p

ren proteinname met

ren se2 se

ren beta2 beta

levelsof met, local(levels)

foreach l of local levels {

di "`l'"

}

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

file open a using "metaresultat\_atherooutcome\_adj.txt", replace write

file write a "met" \_tab "beta" \_tab "se" \_tab "p" \_tab "I\_sq" \_n

foreach l of local levels {

metan beta se if met=="`l'", nograph fixedi

file write a "`l'" \_tab (r(ES)) \_tab (r(seES)) \_tab (2\*normal(-abs((r(ES))/(r(seES))))) \_tab (r(i\_sq)) \_n

}

file close a

clear

cd "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

insheet using "metaresultat\_atherooutcome\_adj.txt"

ren met protein

ren beta beta2

ren se se2

ren p p2

ren i\_sq i\_sq2

sort protein

save "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/metaresultat\_atherooutcome\_adj.dta", replace

\*slå ihop till en tabell

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/metaresultat\_atherooutcome\_unadj.dta", clear

merge protein using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/metaresultat\_atherooutcome\_adj.dta"

tab \_merge

drop \_merge

sort p1

sort protein

merge protein using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/combined outcome\_MDC\_FDRpos\_proteinname.dta"

tab \_merge

drop if \_merge!=3

drop \_merge

sort p1

gen radnummer=\_n

gen vv3= 0.05\*(radnummer/37)

gen FDRyes=0

replace FDRyes=1 if p1 <vv3

keep if FDRyes==1

drop radnummer vv3 FDRyes

gen cilow1=beta1-se1\*1.96

gen cihigh1=beta1+se1\*1.96

gen cilow2=beta2-se2\*1.96

gen cihigh2=beta2+se2\*1.96

replace beta1=exp(beta1)

replace cilow1=exp(cilow1)

replace cihigh1=exp(cihigh1)

replace beta2=exp(beta2)

replace cilow2=exp(cilow2)

replace cihigh2=exp(cihigh2)

drop i\_sq1 i\_sq2

drop se1 se2

order protein beta1 cilow1 cihigh1 p1 beta2 cilow2 cihigh2 p2

sort p1

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* MMP12 (4 st, 1 cis)

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/SCALLOP proteininstrument.dta"

keep if name=="MMP-12"

drop n

\*replace rsid="rs1050317" if rsid=="rs9264664" //byter ut mot proxy

sort rsid

merge rsid using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/GWAS results IMT.dta"

tab \_merge

drop if \_merge!=3 // (alla 4 kvar)

list rsid

keep rsid effect\_allele\_exposure other\_allele\_exposure eaf\_exposure beta\_exposure se\_exposure possible\_cis effect\_allele\_outcome other\_allele\_outcome eaf\_outcome beta\_outcome se\_outcome

\*imt

cd "//Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

file open table2 using "Regression MR results MMP12 vs IMT.txt", replace write

file write table2 "Test" \_tab "Beta" \_tab "CIlow" \_tab "CIhigh" \_tab "P-value" \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //MR Egger med Q

file write table2 "MR Egger" \_tab (round(\_b[slope]),0.0001) \_tab (round(\_b[slope]-1.96\*\_se[slope]),0.0001) \_tab (round(\_b[slope]+1.96\*\_se[slope]),0.0001) \_tab (round(2\*(1-normal(abs(\_b[slope]/\_se[slope]))),0.0000000000001)) \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], ivw fe //IVW

file write table2 "IVW" \_tab (round(\_b[beta\_exposure]),0.0001) \_tab (round(\_b[beta\_exposure]-1.96\*\_se[beta\_exposure]),0.0001) \_tab (round(\_b[beta\_exposure]+1.96\*\_se[beta\_exposure]),0.001) \_tab (round(2\*(1-normal(abs(\_b[beta\_exposure]/\_se[beta\_exposure]))),0.0000000000001)) \_n

mrmedian beta\_outcome se\_outcome beta\_exposure se\_exposure, weighted // Weighted median

file write table2 "Weighted median" \_tab (round(\_b[beta]),0.0001) \_tab (round(\_b[beta]-1.96\*\_se[beta]),0.0001) \_tab (round(\_b[beta]+1.96\*\_se[beta]),0.001) \_tab (round(2\*(1-normal(abs(\_b[beta]/\_se[beta]))),0.0000000000001)) \_n

file write table2 "Heterogeneity" \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //MR Egger med Q

file write table2 "Pleiotropy" \_tab (round(\_b[\_cons]),0.0001) \_tab (round(\_b[\_cons]-1.96\*\_se[\_cons]),0.0001) \_tab (round(\_b[\_cons]+1.96\*\_se[\_cons]),0.001) \_tab (round(2\*(1-normal(abs(\_b[\_cons]/\_se[\_cons]))),0.0000000000001)) \_n

file close table2

mrivests beta\_outcome se\_outcome beta\_exposure se\_exposure, generate(ivest ivse) //genererar causal estimates och se, mregger funkar ej med 2 SNPs, behövs 3.

metan ivest ivse, fixed nograph

keep if possible\_cis=="Y" //rrs72981675

mrratio beta\_outcome se\_outcome beta\_exposure se\_exposure

\*plaque

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/SCALLOP proteininstrument.dta"

keep if name=="MMP-12"

drop n

\*replace rsid="rs1050317" if rsid=="rs9264664" //byter ut mot proxy

sort rsid

merge rsid using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/GWAS results plaque.dta"

tab \_merge

drop if \_merge!=3 // (alla 4 kvar)

list rsid

keep rsid effect\_allele\_exposure other\_allele\_exposure eaf\_exposure beta\_exposure se\_exposure possible\_cis effect\_allele\_outcome other\_allele\_outcome eaf\_outcome beta\_outcome se\_outcome

cd "//Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

file open table2 using "Regression MR results MMP12 vs plaque.txt", replace write

file write table2 "Test" \_tab "Beta" \_tab "CIlow" \_tab "CIhigh" \_tab "P-value" \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //MR Egger med Q

file write table2 "MR Egger" \_tab (round(\_b[slope]),0.0001) \_tab (round(\_b[slope]-1.96\*\_se[slope]),0.0001) \_tab (round(\_b[slope]+1.96\*\_se[slope]),0.0001) \_tab (round(2\*(1-normal(abs(\_b[slope]/\_se[slope]))),0.0000000000001)) \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], ivw fe //IVW

file write table2 "IVW" \_tab (round(\_b[beta\_exposure]),0.0001) \_tab (round(\_b[beta\_exposure]-1.96\*\_se[beta\_exposure]),0.0001) \_tab (round(\_b[beta\_exposure]+1.96\*\_se[beta\_exposure]),0.001) \_tab (round(2\*(1-normal(abs(\_b[beta\_exposure]/\_se[beta\_exposure]))),0.0000000000001)) \_n

mrmedian beta\_outcome se\_outcome beta\_exposure se\_exposure, weighted // Weighted median

file write table2 "Weighted median" \_tab (round(\_b[beta]),0.0001) \_tab (round(\_b[beta]-1.96\*\_se[beta]),0.0001) \_tab (round(\_b[beta]+1.96\*\_se[beta]),0.001) \_tab (round(2\*(1-normal(abs(\_b[beta]/\_se[beta]))),0.0000000000001)) \_n

file write table2 "Heterogeneity" \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //MR Egger med Q

file write table2 "Pleiotropy" \_tab (round(\_b[\_cons]),0.0001) \_tab (round(\_b[\_cons]-1.96\*\_se[\_cons]),0.0001) \_tab (round(\_b[\_cons]+1.96\*\_se[\_cons]),0.001) \_tab (round(2\*(1-normal(abs(\_b[\_cons]/\_se[\_cons]))),0.0000000000001)) \_n

file close table2

mrivests beta\_outcome se\_outcome beta\_exposure se\_exposure, generate(ivest ivse) //genererar causal estimates och se, mregger funkar ej med 2 SNPs, behövs 3.

keep if possible\_cis=="Y" //rs148339496

mrratio beta\_outcome se\_outcome beta\_exposure se\_exposure

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* GAL (4 st alla trans)

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/SCALLOP proteininstrument.dta"

keep if name=="GAL"

drop n

\*replace rsid="rs1050317" if rsid=="rs9264664" //byter ut mot proxy

sort rsid

merge rsid using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/GWAS results IMT.dta"

tab \_merge

drop if \_merge!=3 // (alla 4 kvar)

list rsid

keep rsid effect\_allele\_exposure other\_allele\_exposure eaf\_exposure beta\_exposure se\_exposure possible\_cis effect\_allele\_outcome other\_allele\_outcome eaf\_outcome beta\_outcome se\_outcome

\*imt

cd "//Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

file open table2 using "Regression MR results GAl vs IMT.txt", replace write

file write table2 "Test" \_tab "Beta" \_tab "CIlow" \_tab "CIhigh" \_tab "P-value" \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //MR Egger med Q

file write table2 "MR Egger" \_tab (round(\_b[slope]),0.0001) \_tab (round(\_b[slope]-1.96\*\_se[slope]),0.0001) \_tab (round(\_b[slope]+1.96\*\_se[slope]),0.0001) \_tab (round(2\*(1-normal(abs(\_b[slope]/\_se[slope]))),0.0000000000001)) \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], ivw fe //IVW

file write table2 "IVW" \_tab (round(\_b[beta\_exposure]),0.0001) \_tab (round(\_b[beta\_exposure]-1.96\*\_se[beta\_exposure]),0.0001) \_tab (round(\_b[beta\_exposure]+1.96\*\_se[beta\_exposure]),0.001) \_tab (round(2\*(1-normal(abs(\_b[beta\_exposure]/\_se[beta\_exposure]))),0.0000000000001)) \_n

mrmedian beta\_outcome se\_outcome beta\_exposure se\_exposure, weighted // Weighted median

file write table2 "Weighted median" \_tab (round(\_b[beta]),0.0001) \_tab (round(\_b[beta]-1.96\*\_se[beta]),0.0001) \_tab (round(\_b[beta]+1.96\*\_se[beta]),0.001) \_tab (round(2\*(1-normal(abs(\_b[beta]/\_se[beta]))),0.0000000000001)) \_n

file write table2 "Heterogeneity" \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //MR Egger med Q

file write table2 "Pleiotropy" \_tab (round(\_b[\_cons]),0.0001) \_tab (round(\_b[\_cons]-1.96\*\_se[\_cons]),0.0001) \_tab (round(\_b[\_cons]+1.96\*\_se[\_cons]),0.001) \_tab (round(2\*(1-normal(abs(\_b[\_cons]/\_se[\_cons]))),0.0000000000001)) \_n

file close table2

\*plaque

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/SCALLOP proteininstrument.dta"

keep if name=="GAL"

drop n

\*replace rsid="rs1050317" if rsid=="rs9264664" //byter ut mot proxy

sort rsid

merge rsid using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/GWAS results plaque.dta"

tab \_merge

drop if \_merge!=3 // (alla 4 kvar)

list rsid

keep rsid effect\_allele\_exposure other\_allele\_exposure eaf\_exposure beta\_exposure se\_exposure possible\_cis effect\_allele\_outcome other\_allele\_outcome eaf\_outcome beta\_outcome se\_outcome

cd "//Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

file open table2 using "Regression MR results GAL vs plaque.txt", replace write

file write table2 "Test" \_tab "Beta" \_tab "CIlow" \_tab "CIhigh" \_tab "P-value" \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //MR Egger med Q

file write table2 "MR Egger" \_tab (round(\_b[slope]),0.0001) \_tab (round(\_b[slope]-1.96\*\_se[slope]),0.0001) \_tab (round(\_b[slope]+1.96\*\_se[slope]),0.0001) \_tab (round(2\*(1-normal(abs(\_b[slope]/\_se[slope]))),0.0000000000001)) \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], ivw fe //IVW

file write table2 "IVW" \_tab (round(\_b[beta\_exposure]),0.0001) \_tab (round(\_b[beta\_exposure]-1.96\*\_se[beta\_exposure]),0.0001) \_tab (round(\_b[beta\_exposure]+1.96\*\_se[beta\_exposure]),0.001) \_tab (round(2\*(1-normal(abs(\_b[beta\_exposure]/\_se[beta\_exposure]))),0.0000000000001)) \_n

mrmedian beta\_outcome se\_outcome beta\_exposure se\_exposure, weighted // Weighted median

file write table2 "Weighted median" \_tab (round(\_b[beta]),0.0001) \_tab (round(\_b[beta]-1.96\*\_se[beta]),0.0001) \_tab (round(\_b[beta]+1.96\*\_se[beta]),0.001) \_tab (round(2\*(1-normal(abs(\_b[beta]/\_se[beta]))),0.0000000000001)) \_n

file write table2 "Heterogeneity" \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //MR Egger med Q

file write table2 "Pleiotropy" \_tab (round(\_b[\_cons]),0.0001) \_tab (round(\_b[\_cons]-1.96\*\_se[\_cons]),0.0001) \_tab (round(\_b[\_cons]+1.96\*\_se[\_cons]),0.001) \_tab (round(2\*(1-normal(abs(\_b[\_cons]/\_se[\_cons]))),0.0000000000001)) \_n

file close table2

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* NT-proBNP (1 cis)

\*sun PMID 21273288

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/SCALLOP proteininstrument.dta"

keep if name=="NT-pro-BNP"

drop n

\*replace rsid="rs1050317" if rsid=="rs9264664" //byter ut mot proxy

sort rsid

merge rsid using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/GWAS results IMT.dta"

tab \_merge

drop if \_merge!=3 // (alla 4 kvar)

list rsid

keep rsid effect\_allele\_exposure other\_allele\_exposure eaf\_exposure beta\_exposure se\_exposure possible\_cis effect\_allele\_outcome other\_allele\_outcome eaf\_outcome beta\_outcome se\_outcome

\*imt

mrivests beta\_outcome se\_outcome beta\_exposure se\_exposure, generate(ivest ivse) //genererar causal estimates och se, mregger funkar ej med 2 SNPs, behövs 3.

mrratio beta\_outcome se\_outcome beta\_exposure se\_exposure

\*plaque

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/SCALLOP proteininstrument.dta"

keep if name=="NT-pro-BNP"

drop n

\*replace rsid="rs1050317" if rsid=="rs9264664" //byter ut mot proxy

sort rsid

merge rsid using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/GWAS results plaque.dta"

tab \_merge

drop if \_merge!=3 // (alla 4 kvar)

list rsid

keep rsid effect\_allele\_exposure other\_allele\_exposure eaf\_exposure beta\_exposure se\_exposure possible\_cis effect\_allele\_outcome other\_allele\_outcome eaf\_outcome beta\_outcome se\_outcome

mrivests beta\_outcome se\_outcome beta\_exposure se\_exposure, generate(ivest ivse) //genererar causal estimates och se, mregger funkar ej med 2 SNPs, behövs 3.

mrratio beta\_outcome se\_outcome beta\_exposure se\_exposure

\*kolla mot meta-stroke

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/SCALLOP proteininstrument.dta"

keep if name=="NT-pro-BNP"

drop n

ren rsid SNP

sort SNP

merge SNP using "/Users/larslind/Lind kopior/Mendelian randomization/Nedladdningar/MEGASTROKE\_ishcemic.dta"

tab \_merge

drop if \_merge!=3 // (alla 4 kvar)

list SNP

ren effect\_allele effect\_allele\_outcome

ren beta beta\_outcome

ren se se\_outcome

ren other\_allele other\_allele\_outcome

ren eaf eaf\_outcome

keep SNP effect\_allele\_exposure other\_allele\_exposure eaf\_exposure beta\_exposure se\_exposure possible\_cis effect\_allele\_outcome other\_allele\_outcome eaf\_outcome beta\_outcome se\_outcome

mrivests beta\_outcome se\_outcome beta\_exposure se\_exposure, generate(ivest ivse) //genererar causal estimates och se, mregger funkar ej med 2 SNPs, behövs 3.

mrratio beta\_outcome se\_outcome beta\_exposure se\_exposure

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* CD40 ( 3 SNPs, varav 2 cis, 1 i exomet)

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/SCALLOP proteininstrument.dta"

keep if name=="CD40"

drop n

\*replace rsid="rs1050317" if rsid=="rs9264664" //byter ut mot proxy

sort rsid

merge rsid using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/GWAS results IMT.dta"

tab \_merge

drop if \_merge!=3 // (alla 4 kvar)

list rsid

keep rsid effect\_allele\_exposure other\_allele\_exposure eaf\_exposure beta\_exposure se\_exposure possible\_cis effect\_allele\_outcome other\_allele\_outcome eaf\_outcome beta\_outcome se\_outcome

\*imt

\*mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //konvergerar ej med 3 SNPs

mrivests beta\_outcome se\_outcome beta\_exposure se\_exposure, generate(ivest ivse) //genererar causal estimates och se, mregger funkar ej med 2 SNPs, behövs 3.

metan ivest ivse, fixed nograph

keep if rsid=="rs4810485" //rrs4810485

mrratio beta\_outcome se\_outcome beta\_exposure se\_exposure

\*plaque

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/SCALLOP proteininstrument.dta"

keep if name=="CD40"

drop n

\*replace rsid="rs1050317" if rsid=="rs9264664" //byter ut mot proxy

sort rsid

merge rsid using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/GWAS results plaque.dta"

tab \_merge

drop if \_merge!=3 // (alla 4 kvar)

list rsid

keep rsid effect\_allele\_exposure other\_allele\_exposure eaf\_exposure beta\_exposure se\_exposure possible\_cis effect\_allele\_outcome other\_allele\_outcome eaf\_outcome beta\_outcome se\_outcome

\*mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //konvergerar ej med 3 SNPs

mrivests beta\_outcome se\_outcome beta\_exposure se\_exposure, generate(ivest ivse) //genererar causal estimates och se, mregger funkar ej med 2 SNPs, behövs 3.

metan ivest ivse, fixed nograph

keep if rsid=="rs4810485" //rrs4810485

mrratio beta\_outcome se\_outcome beta\_exposure se\_exposure

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*. MCP-1 (6 SNP, 1 cis)

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/SCALLOP proteininstrument.dta"

keep if name=="MCP-1"

drop n

\*replace rsid="rs1050317" if rsid=="rs9264664" //byter ut mot proxy

sort rsid

merge rsid using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/GWAS results IMT.dta"

tab \_merge

drop if \_merge!=3 // (alla 6 kvar)

list rsid

keep rsid effect\_allele\_exposure other\_allele\_exposure eaf\_exposure beta\_exposure se\_exposure possible\_cis effect\_allele\_outcome other\_allele\_outcome eaf\_outcome beta\_outcome se\_outcome

\*imt

cd "//Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

file open table2 using "Regression MR results MCP1 vs IMT.txt", replace write

file write table2 "Test" \_tab "Beta" \_tab "CIlow" \_tab "CIhigh" \_tab "P-value" \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //MR Egger med Q

file write table2 "MR Egger" \_tab (round(\_b[slope]),0.0001) \_tab (round(\_b[slope]-1.96\*\_se[slope]),0.0001) \_tab (round(\_b[slope]+1.96\*\_se[slope]),0.0001) \_tab (round(2\*(1-normal(abs(\_b[slope]/\_se[slope]))),0.0000000000001)) \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], ivw fe //IVW

file write table2 "IVW" \_tab (round(\_b[beta\_exposure]),0.0001) \_tab (round(\_b[beta\_exposure]-1.96\*\_se[beta\_exposure]),0.0001) \_tab (round(\_b[beta\_exposure]+1.96\*\_se[beta\_exposure]),0.001) \_tab (round(2\*(1-normal(abs(\_b[beta\_exposure]/\_se[beta\_exposure]))),0.0000000000001)) \_n

mrmedian beta\_outcome se\_outcome beta\_exposure se\_exposure, weighted // Weighted median

file write table2 "Weighted median" \_tab (round(\_b[beta]),0.0001) \_tab (round(\_b[beta]-1.96\*\_se[beta]),0.0001) \_tab (round(\_b[beta]+1.96\*\_se[beta]),0.001) \_tab (round(2\*(1-normal(abs(\_b[beta]/\_se[beta]))),0.0000000000001)) \_n

file write table2 "Heterogeneity" \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //MR Egger med Q

file write table2 "Pleiotropy" \_tab (round(\_b[\_cons]),0.0001) \_tab (round(\_b[\_cons]-1.96\*\_se[\_cons]),0.0001) \_tab (round(\_b[\_cons]+1.96\*\_se[\_cons]),0.001) \_tab (round(2\*(1-normal(abs(\_b[\_cons]/\_se[\_cons]))),0.0000000000001)) \_n

file close table2

mrivests beta\_outcome se\_outcome beta\_exposure se\_exposure, generate(ivest ivse) //genererar causal estimates och se, mregger funkar ej med 2 SNPs, behövs 3.

metan ivest ivse, fixed nograph

keep if possible\_cis=="Y" //rrs72981675

mrratio beta\_outcome se\_outcome beta\_exposure se\_exposure

\*plaque

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/SCALLOP proteininstrument.dta"

keep if name=="MCP-1"

drop n

\*replace rsid="rs1050317" if rsid=="rs9264664" //byter ut mot proxy

sort rsid

merge rsid using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/GWAS results plaque.dta"

tab \_merge

drop if \_merge!=3 // (alla 4 kvar)

list rsid

keep rsid effect\_allele\_exposure other\_allele\_exposure eaf\_exposure beta\_exposure se\_exposure possible\_cis effect\_allele\_outcome other\_allele\_outcome eaf\_outcome beta\_outcome se\_outcome

cd "//Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

file open table2 using "Regression MR results MCP1 vs plaque.txt", replace write

file write table2 "Test" \_tab "Beta" \_tab "CIlow" \_tab "CIhigh" \_tab "P-value" \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //MR Egger med Q

file write table2 "MR Egger" \_tab (round(\_b[slope]),0.0001) \_tab (round(\_b[slope]-1.96\*\_se[slope]),0.0001) \_tab (round(\_b[slope]+1.96\*\_se[slope]),0.0001) \_tab (round(2\*(1-normal(abs(\_b[slope]/\_se[slope]))),0.0000000000001)) \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], ivw fe //IVW

file write table2 "IVW" \_tab (round(\_b[beta\_exposure]),0.0001) \_tab (round(\_b[beta\_exposure]-1.96\*\_se[beta\_exposure]),0.0001) \_tab (round(\_b[beta\_exposure]+1.96\*\_se[beta\_exposure]),0.001) \_tab (round(2\*(1-normal(abs(\_b[beta\_exposure]/\_se[beta\_exposure]))),0.0000000000001)) \_n

mrmedian beta\_outcome se\_outcome beta\_exposure se\_exposure, weighted // Weighted median

file write table2 "Weighted median" \_tab (round(\_b[beta]),0.0001) \_tab (round(\_b[beta]-1.96\*\_se[beta]),0.0001) \_tab (round(\_b[beta]+1.96\*\_se[beta]),0.001) \_tab (round(2\*(1-normal(abs(\_b[beta]/\_se[beta]))),0.0000000000001)) \_n

file write table2 "Heterogeneity" \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //MR Egger med Q

file write table2 "Pleiotropy" \_tab (round(\_b[\_cons]),0.0001) \_tab (round(\_b[\_cons]-1.96\*\_se[\_cons]),0.0001) \_tab (round(\_b[\_cons]+1.96\*\_se[\_cons]),0.001) \_tab (round(2\*(1-normal(abs(\_b[\_cons]/\_se[\_cons]))),0.0000000000001)) \_n

file close table2

mrivests beta\_outcome se\_outcome beta\_exposure se\_exposure, generate(ivest ivse) //genererar causal estimates och se, mregger funkar ej med 2 SNPs, behövs 3.

keep if possible\_cis=="Y" //rs148339496

mrratio beta\_outcome se\_outcome beta\_exposure se\_exposure

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* ECP (2 st varav 1 cis)

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/SCALLOP proteininstrument.dta"

keep if name=="ECP"

drop n

\*replace rsid="rs1050317" if rsid=="rs9264664" //byter ut mot proxy

sort rsid

merge rsid using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/GWAS results IMT.dta"

tab \_merge

drop if \_merge!=3 // (alla 6 kvar)

list rsid

keep rsid effect\_allele\_exposure other\_allele\_exposure eaf\_exposure beta\_exposure se\_exposure possible\_cis effect\_allele\_outcome other\_allele\_outcome eaf\_outcome beta\_outcome se\_outcome

\*imt

\*mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //konvergerar ej med 3 SNPs

mrivests beta\_outcome se\_outcome beta\_exposure se\_exposure, generate(ivest ivse) //genererar causal estimates och se, mregger funkar ej med 2 SNPs, behövs 3.

metan ivest ivse, fixed nograph

keep if possible\_cis=="Y" //rs148339496

mrratio beta\_outcome se\_outcome beta\_exposure se\_exposure

\*plaque

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/SCALLOP proteininstrument.dta"

keep if name=="ECP"

drop n

\*replace rsid="rs1050317" if rsid=="rs9264664" //byter ut mot proxy

sort rsid

merge rsid using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/GWAS results plaque.dta"

tab \_merge

drop if \_merge!=3 // (alla 4 kvar)

list rsid

keep rsid effect\_allele\_exposure other\_allele\_exposure eaf\_exposure beta\_exposure se\_exposure possible\_cis effect\_allele\_outcome other\_allele\_outcome eaf\_outcome beta\_outcome se\_outcome

\*mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //konvergerar ej med 3 SNPs

mrivests beta\_outcome se\_outcome beta\_exposure se\_exposure, generate(ivest ivse) //genererar causal estimates och se, mregger funkar ej med 2 SNPs, behövs 3.

metan ivest ivse, fixed nograph

keep if possible\_cis=="Y" //rs148339496

mrratio beta\_outcome se\_outcome beta\_exposure se\_exposure

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* CASP-8 ( 2 st varav en cis)

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/SCALLOP proteininstrument.dta"

keep if name=="CASP-8"

drop n

\*replace rsid="rs1050317" if rsid=="rs9264664" //byter ut mot proxy

sort rsid

merge rsid using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/GWAS results IMT.dta"

tab \_merge

drop if \_merge!=3 // (alla 6 kvar)

list rsid

keep rsid effect\_allele\_exposure other\_allele\_exposure eaf\_exposure beta\_exposure se\_exposure possible\_cis effect\_allele\_outcome other\_allele\_outcome eaf\_outcome beta\_outcome se\_outcome

\*imt

\*mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //konvergerar ej med 3 SNPs

mrivests beta\_outcome se\_outcome beta\_exposure se\_exposure, generate(ivest ivse) //genererar causal estimates och se, mregger funkar ej med 2 SNPs, behövs 3.

metan ivest ivse, fixed nograph

keep if possible\_cis=="Y" //rs148339496

mrratio beta\_outcome se\_outcome beta\_exposure se\_exposure

\*plaque

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/SCALLOP proteininstrument.dta"

keep if name=="CASP-8"

drop n

\*replace rsid="rs1050317" if rsid=="rs9264664" //byter ut mot proxy

sort rsid

merge rsid using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/GWAS results plaque.dta"

tab \_merge

drop if \_merge!=3 // (alla 4 kvar)

list rsid

keep rsid effect\_allele\_exposure other\_allele\_exposure eaf\_exposure beta\_exposure se\_exposure possible\_cis effect\_allele\_outcome other\_allele\_outcome eaf\_outcome beta\_outcome se\_outcome

\*mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //konvergerar ej med 3 SNPs

mrivests beta\_outcome se\_outcome beta\_exposure se\_exposure, generate(ivest ivse) //genererar causal estimates och se, mregger funkar ej med 2 SNPs, behövs 3.

metan ivest ivse, fixed nograph

keep if possible\_cis=="Y" //rs148339496

mrratio beta\_outcome se\_outcome beta\_exposure se\_exposure

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* PAPPA. ((11 st varav 1 cis)

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/SCALLOP proteininstrument.dta"

keep if name=="PAPPA"

drop n

\*replace rsid="rs1050317" if rsid=="rs9264664" //byter ut mot proxy

sort rsid

merge rsid using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/GWAS results IMT.dta"

tab \_merge

drop if \_merge!=3 // (alla 6 kvar)

list rsid

keep rsid effect\_allele\_exposure other\_allele\_exposure eaf\_exposure beta\_exposure se\_exposure possible\_cis effect\_allele\_outcome other\_allele\_outcome eaf\_outcome beta\_outcome se\_outcome

\*imt

cd "//Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

file open table2 using "Regression MR results PAPPA vs IMT.txt", replace write

file write table2 "Test" \_tab "Beta" \_tab "CIlow" \_tab "CIhigh" \_tab "P-value" \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //MR Egger med Q

file write table2 "MR Egger" \_tab (round(\_b[slope]),0.0001) \_tab (round(\_b[slope]-1.96\*\_se[slope]),0.0001) \_tab (round(\_b[slope]+1.96\*\_se[slope]),0.0001) \_tab (round(2\*(1-normal(abs(\_b[slope]/\_se[slope]))),0.0000000000001)) \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], ivw fe //IVW

file write table2 "IVW" \_tab (round(\_b[beta\_exposure]),0.0001) \_tab (round(\_b[beta\_exposure]-1.96\*\_se[beta\_exposure]),0.0001) \_tab (round(\_b[beta\_exposure]+1.96\*\_se[beta\_exposure]),0.001) \_tab (round(2\*(1-normal(abs(\_b[beta\_exposure]/\_se[beta\_exposure]))),0.0000000000001)) \_n

mrmedian beta\_outcome se\_outcome beta\_exposure se\_exposure, weighted // Weighted median

file write table2 "Weighted median" \_tab (round(\_b[beta]),0.0001) \_tab (round(\_b[beta]-1.96\*\_se[beta]),0.0001) \_tab (round(\_b[beta]+1.96\*\_se[beta]),0.001) \_tab (round(2\*(1-normal(abs(\_b[beta]/\_se[beta]))),0.0000000000001)) \_n

file write table2 "Heterogeneity" \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //MR Egger med Q

file write table2 "Pleiotropy" \_tab (round(\_b[\_cons]),0.0001) \_tab (round(\_b[\_cons]-1.96\*\_se[\_cons]),0.0001) \_tab (round(\_b[\_cons]+1.96\*\_se[\_cons]),0.001) \_tab (round(2\*(1-normal(abs(\_b[\_cons]/\_se[\_cons]))),0.0000000000001)) \_n

file close table2

mrivests beta\_outcome se\_outcome beta\_exposure se\_exposure, generate(ivest ivse) //genererar causal estimates och se, mregger funkar ej med 2 SNPs, behövs 3.

keep if possible\_cis=="Y" //rrs72981675

mrratio beta\_outcome se\_outcome beta\_exposure se\_exposure

\*plaque

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/SCALLOP proteininstrument.dta"

keep if name=="PAPPA"

drop n

\*replace rsid="rs1050317" if rsid=="rs9264664" //byter ut mot proxy

sort rsid

merge rsid using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/GWAS results plaque.dta"

tab \_merge

drop if \_merge!=3 // (alla 4 kvar)

list rsid

keep rsid effect\_allele\_exposure other\_allele\_exposure eaf\_exposure beta\_exposure se\_exposure possible\_cis effect\_allele\_outcome other\_allele\_outcome eaf\_outcome beta\_outcome se\_outcome

cd "//Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

file open table2 using "Regression MR results PAPPA vs plaque.txt", replace write

file write table2 "Test" \_tab "Beta" \_tab "CIlow" \_tab "CIhigh" \_tab "P-value" \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //MR Egger med Q

file write table2 "MR Egger" \_tab (round(\_b[slope]),0.0001) \_tab (round(\_b[slope]-1.96\*\_se[slope]),0.0001) \_tab (round(\_b[slope]+1.96\*\_se[slope]),0.0001) \_tab (round(2\*(1-normal(abs(\_b[slope]/\_se[slope]))),0.0000000000001)) \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], ivw fe //IVW

file write table2 "IVW" \_tab (round(\_b[beta\_exposure]),0.0001) \_tab (round(\_b[beta\_exposure]-1.96\*\_se[beta\_exposure]),0.0001) \_tab (round(\_b[beta\_exposure]+1.96\*\_se[beta\_exposure]),0.001) \_tab (round(2\*(1-normal(abs(\_b[beta\_exposure]/\_se[beta\_exposure]))),0.0000000000001)) \_n

mrmedian beta\_outcome se\_outcome beta\_exposure se\_exposure, weighted // Weighted median

file write table2 "Weighted median" \_tab (round(\_b[beta]),0.0001) \_tab (round(\_b[beta]-1.96\*\_se[beta]),0.0001) \_tab (round(\_b[beta]+1.96\*\_se[beta]),0.001) \_tab (round(2\*(1-normal(abs(\_b[beta]/\_se[beta]))),0.0000000000001)) \_n

file write table2 "Heterogeneity" \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //MR Egger med Q

file write table2 "Pleiotropy" \_tab (round(\_b[\_cons]),0.0001) \_tab (round(\_b[\_cons]-1.96\*\_se[\_cons]),0.0001) \_tab (round(\_b[\_cons]+1.96\*\_se[\_cons]),0.001) \_tab (round(2\*(1-normal(abs(\_b[\_cons]/\_se[\_cons]))),0.0000000000001)) \_n

file close table2

mrivests beta\_outcome se\_outcome beta\_exposure se\_exposure, generate(ivest ivse) //genererar causal estimates och se, mregger funkar ej med 2 SNPs, behövs 3.

keep if possible\_cis=="Y" //rs148339496

mrratio beta\_outcome se\_outcome beta\_exposure se\_exposure

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* CD40L (1 st i trans)

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/SCALLOP proteininstrument.dta"

keep if name=="CD40-L"

drop n

\*replace rsid="rs1050317" if rsid=="rs9264664" //byter ut mot proxy

sort rsid

merge rsid using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/GWAS results IMT.dta"

tab \_merge

drop if \_merge!=3 // (alla 6 kvar)

list rsid

keep rsid effect\_allele\_exposure other\_allele\_exposure eaf\_exposure beta\_exposure se\_exposure possible\_cis effect\_allele\_outcome other\_allele\_outcome eaf\_outcome beta\_outcome se\_outcome

\*imt

\*mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //konvergerar ej med 3 SNPs

mrivests beta\_outcome se\_outcome beta\_exposure se\_exposure, generate(ivest ivse) //genererar causal estimates och se, mregger funkar ej med 2 SNPs, behövs 3.

mrratio beta\_outcome se\_outcome beta\_exposure se\_exposure

\*plaque

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/SCALLOP proteininstrument.dta"

keep if name=="CD40-L"

drop n

\*replace rsid="rs1050317" if rsid=="rs9264664" //byter ut mot proxy

sort rsid

merge rsid using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/GWAS results plaque.dta"

tab \_merge

drop if \_merge!=3 // (alla 4 kvar)

list rsid

keep rsid effect\_allele\_exposure other\_allele\_exposure eaf\_exposure beta\_exposure se\_exposure possible\_cis effect\_allele\_outcome other\_allele\_outcome eaf\_outcome beta\_outcome se\_outcome

\*mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //konvergerar ej med 3 SNPs

mrivests beta\_outcome se\_outcome beta\_exposure se\_exposure, generate(ivest ivse) //genererar causal estimates och se, mregger funkar ej med 2 SNPs, behövs 3.

mrratio beta\_outcome se\_outcome beta\_exposure se\_exposure

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*. HSP-27 (2 i cis)

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/SCALLOP proteininstrument.dta"

keep if name=="HSP 27"

drop n

\*replace rsid="rs1050317" if rsid=="rs9264664" //byter ut mot proxy

sort rsid

merge rsid using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/GWAS results IMT.dta"

tab \_merge

drop if \_merge!=3 // (alla 6 kvar)

list rsid

keep rsid effect\_allele\_exposure other\_allele\_exposure eaf\_exposure beta\_exposure se\_exposure possible\_cis effect\_allele\_outcome other\_allele\_outcome eaf\_outcome beta\_outcome se\_outcome

\*imt

\*mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //konvergerar ej med 3 SNPs

mrivests beta\_outcome se\_outcome beta\_exposure se\_exposure, generate(ivest ivse) //genererar causal estimates och se, mregger funkar ej med 2 SNPs, behövs 3.

metan ivest ivse, fixed nograph

keep if rsid=="rs2868371" //rs148339496

mrratio beta\_outcome se\_outcome beta\_exposure se\_exposure

\*plaque

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/SCALLOP proteininstrument.dta"

keep if name=="HSP 27"

drop n

\*replace rsid="rs1050317" if rsid=="rs9264664" //byter ut mot proxy

sort rsid

merge rsid using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/GWAS results plaque.dta"

tab \_merge

drop if \_merge!=3 // (alla 4 kvar)

list rsid

keep rsid effect\_allele\_exposure other\_allele\_exposure eaf\_exposure beta\_exposure se\_exposure possible\_cis effect\_allele\_outcome other\_allele\_outcome eaf\_outcome beta\_outcome se\_outcome

\*mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //konvergerar ej med 3 SNPs

mrivests beta\_outcome se\_outcome beta\_exposure se\_exposure, generate(ivest ivse) //genererar causal estimates och se, mregger funkar ej med 2 SNPs, behövs 3.

metan ivest ivse, fixed nograph

keep if rsid=="rs2868371" //rs148339496

mrratio beta\_outcome se\_outcome beta\_exposure se\_exposure

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*. TM (5 varav 2 cis)

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/SCALLOP proteininstrument.dta"

keep if name=="TM"

drop n

\*replace rsid="rs1050317" if rsid=="rs9264664" //byter ut mot proxy

sort rsid

merge rsid using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/GWAS results IMT.dta"

tab \_merge

drop if \_merge!=3 // (alla 6 kvar)

list rsid

keep rsid effect\_allele\_exposure other\_allele\_exposure eaf\_exposure beta\_exposure se\_exposure possible\_cis effect\_allele\_outcome other\_allele\_outcome eaf\_outcome beta\_outcome se\_outcome

\*imt

cd "//Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

file open table2 using "Regression MR results TM vs IMT.txt", replace write

file write table2 "Test" \_tab "Beta" \_tab "CIlow" \_tab "CIhigh" \_tab "P-value" \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //MR Egger med Q

file write table2 "MR Egger" \_tab (round(\_b[slope]),0.0001) \_tab (round(\_b[slope]-1.96\*\_se[slope]),0.0001) \_tab (round(\_b[slope]+1.96\*\_se[slope]),0.0001) \_tab (round(2\*(1-normal(abs(\_b[slope]/\_se[slope]))),0.0000000000001)) \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], ivw fe //IVW

file write table2 "IVW" \_tab (round(\_b[beta\_exposure]),0.0001) \_tab (round(\_b[beta\_exposure]-1.96\*\_se[beta\_exposure]),0.0001) \_tab (round(\_b[beta\_exposure]+1.96\*\_se[beta\_exposure]),0.001) \_tab (round(2\*(1-normal(abs(\_b[beta\_exposure]/\_se[beta\_exposure]))),0.0000000000001)) \_n

mrmedian beta\_outcome se\_outcome beta\_exposure se\_exposure, weighted // Weighted median

file write table2 "Weighted median" \_tab (round(\_b[beta]),0.0001) \_tab (round(\_b[beta]-1.96\*\_se[beta]),0.0001) \_tab (round(\_b[beta]+1.96\*\_se[beta]),0.001) \_tab (round(2\*(1-normal(abs(\_b[beta]/\_se[beta]))),0.0000000000001)) \_n

file write table2 "Heterogeneity" \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //MR Egger med Q

file write table2 "Pleiotropy" \_tab (round(\_b[\_cons]),0.0001) \_tab (round(\_b[\_cons]-1.96\*\_se[\_cons]),0.0001) \_tab (round(\_b[\_cons]+1.96\*\_se[\_cons]),0.001) \_tab (round(2\*(1-normal(abs(\_b[\_cons]/\_se[\_cons]))),0.0000000000001)) \_n

file close table2

mrivests beta\_outcome se\_outcome beta\_exposure se\_exposure, generate(ivest ivse) //genererar causal estimates och se, mregger funkar ej med 2 SNPs, behövs 3.

keep if rsid=="rs1042579" //rrs72981675

mrratio beta\_outcome se\_outcome beta\_exposure se\_exposure

\*plaque

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/SCALLOP proteininstrument.dta"

keep if name=="TM"

drop n

\*replace rsid="rs1050317" if rsid=="rs9264664" //byter ut mot proxy

sort rsid

merge rsid using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/GWAS results plaque.dta"

tab \_merge

drop if \_merge!=3 // (alla 4 kvar)

list rsid

keep rsid effect\_allele\_exposure other\_allele\_exposure eaf\_exposure beta\_exposure se\_exposure possible\_cis effect\_allele\_outcome other\_allele\_outcome eaf\_outcome beta\_outcome se\_outcome

cd "//Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

file open table2 using "Regression MR results TM vs plaque.txt", replace write

file write table2 "Test" \_tab "Beta" \_tab "CIlow" \_tab "CIhigh" \_tab "P-value" \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //MR Egger med Q

file write table2 "MR Egger" \_tab (round(\_b[slope]),0.0001) \_tab (round(\_b[slope]-1.96\*\_se[slope]),0.0001) \_tab (round(\_b[slope]+1.96\*\_se[slope]),0.0001) \_tab (round(2\*(1-normal(abs(\_b[slope]/\_se[slope]))),0.0000000000001)) \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], ivw fe //IVW

file write table2 "IVW" \_tab (round(\_b[beta\_exposure]),0.0001) \_tab (round(\_b[beta\_exposure]-1.96\*\_se[beta\_exposure]),0.0001) \_tab (round(\_b[beta\_exposure]+1.96\*\_se[beta\_exposure]),0.001) \_tab (round(2\*(1-normal(abs(\_b[beta\_exposure]/\_se[beta\_exposure]))),0.0000000000001)) \_n

mrmedian beta\_outcome se\_outcome beta\_exposure se\_exposure, weighted // Weighted median

file write table2 "Weighted median" \_tab (round(\_b[beta]),0.0001) \_tab (round(\_b[beta]-1.96\*\_se[beta]),0.0001) \_tab (round(\_b[beta]+1.96\*\_se[beta]),0.001) \_tab (round(2\*(1-normal(abs(\_b[beta]/\_se[beta]))),0.0000000000001)) \_n

file write table2 "Heterogeneity" \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //MR Egger med Q

file write table2 "Pleiotropy" \_tab (round(\_b[\_cons]),0.0001) \_tab (round(\_b[\_cons]-1.96\*\_se[\_cons]),0.0001) \_tab (round(\_b[\_cons]+1.96\*\_se[\_cons]),0.001) \_tab (round(2\*(1-normal(abs(\_b[\_cons]/\_se[\_cons]))),0.0000000000001)) \_n

file close table2

mrivests beta\_outcome se\_outcome beta\_exposure se\_exposure, generate(ivest ivse) //genererar causal estimates och se, mregger funkar ej med 2 SNPs, behövs 3.

keep if rsid=="rs1042579" //rrs72981675

mrratio beta\_outcome se\_outcome beta\_exposure se\_exposure

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* GDF-15 (1 cis)

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/SCALLOP proteininstrument.dta"

keep if name=="GDF-15"

drop n

\*replace rsid="rs1050317" if rsid=="rs9264664" //byter ut mot proxy

sort rsid

merge rsid using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/GWAS results IMT.dta"

tab \_merge

drop if \_merge!=3 // (alla 6 kvar)

list rsid

\*imt

\*mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //konvergerar ej med 3 SNPs

mrivests beta\_outcome se\_outcome beta\_exposure se\_exposure, generate(ivest ivse) //genererar causal estimates och se, mregger funkar ej med 2 SNPs, behövs 3.

mrratio beta\_outcome se\_outcome beta\_exposure se\_exposure

\*plaque

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/SCALLOP proteininstrument.dta"

keep if name=="GDF-15"

drop n

\*replace rsid="rs1050317" if rsid=="rs9264664" //byter ut mot proxy

sort rsid

merge rsid using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/GWAS results plaque.dta"

tab \_merge

drop if \_merge!=3 // (alla 4 kvar)

list rsid

keep rsid effect\_allele\_exposure other\_allele\_exposure eaf\_exposure beta\_exposure se\_exposure possible\_cis effect\_allele\_outcome other\_allele\_outcome eaf\_outcome beta\_outcome se\_outcome

\*mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //konvergerar ej med 3 SNPs

mrivests beta\_outcome se\_outcome beta\_exposure se\_exposure, generate(ivest ivse) //genererar causal estimates och se, mregger funkar ej med 2 SNPs, behövs 3.

mrratio beta\_outcome se\_outcome beta\_exposure se\_exposure

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*. TIM-1=KIM-1 (8 varav 1 cis)

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/SCALLOP proteininstrument.dta"

keep if name=="KIM-1"

drop n

drop if rsid=="rs147992984"

\*replace rsid="rs1050317" if rsid=="rs9264664" //byter ut mot proxy

sort rsid

merge rsid using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/GWAS results IMT.dta"

tab \_merge

drop if \_merge!=3 // (alla 6 kvar)

list rsid

keep rsid effect\_allele\_exposure other\_allele\_exposure eaf\_exposure beta\_exposure se\_exposure possible\_cis effect\_allele\_outcome other\_allele\_outcome eaf\_outcome beta\_outcome se\_outcome

\*imt

cd "//Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

file open table2 using "Regression MR results TIM-1 vs IMT.txt", replace write

file write table2 "Test" \_tab "Beta" \_tab "CIlow" \_tab "CIhigh" \_tab "P-value" \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //MR Egger med Q

file write table2 "MR Egger" \_tab (round(\_b[slope]),0.0001) \_tab (round(\_b[slope]-1.96\*\_se[slope]),0.0001) \_tab (round(\_b[slope]+1.96\*\_se[slope]),0.0001) \_tab (round(2\*(1-normal(abs(\_b[slope]/\_se[slope]))),0.0000000000001)) \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], ivw fe //IVW

file write table2 "IVW" \_tab (round(\_b[beta\_exposure]),0.0001) \_tab (round(\_b[beta\_exposure]-1.96\*\_se[beta\_exposure]),0.0001) \_tab (round(\_b[beta\_exposure]+1.96\*\_se[beta\_exposure]),0.001) \_tab (round(2\*(1-normal(abs(\_b[beta\_exposure]/\_se[beta\_exposure]))),0.0000000000001)) \_n

mrmedian beta\_outcome se\_outcome beta\_exposure se\_exposure, weighted // Weighted median

file write table2 "Weighted median" \_tab (round(\_b[beta]),0.0001) \_tab (round(\_b[beta]-1.96\*\_se[beta]),0.0001) \_tab (round(\_b[beta]+1.96\*\_se[beta]),0.001) \_tab (round(2\*(1-normal(abs(\_b[beta]/\_se[beta]))),0.0000000000001)) \_n

file write table2 "Heterogeneity" \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //MR Egger med Q

file write table2 "Pleiotropy" \_tab (round(\_b[\_cons]),0.0001) \_tab (round(\_b[\_cons]-1.96\*\_se[\_cons]),0.0001) \_tab (round(\_b[\_cons]+1.96\*\_se[\_cons]),0.001) \_tab (round(2\*(1-normal(abs(\_b[\_cons]/\_se[\_cons]))),0.0000000000001)) \_n

file close table2

mrivests beta\_outcome se\_outcome beta\_exposure se\_exposure, generate(ivest ivse) //genererar causal estimates och se, mregger funkar ej med 2 SNPs, behövs 3.

keep if rsid=="rs6555820" //rrs72981675

mrratio beta\_outcome se\_outcome beta\_exposure se\_exposure

\*plaque

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/SCALLOP proteininstrument.dta"

keep if name=="KIM-1"

drop n

drop if rsid=="rs147992984"

\*replace rsid="rs1050317" if rsid=="rs9264664" //byter ut mot proxy

sort rsid

merge rsid using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/GWAS results plaque.dta"

tab \_merge

drop if \_merge!=3 // (alla 4 kvar)

list rsid

keep rsid effect\_allele\_exposure other\_allele\_exposure eaf\_exposure beta\_exposure se\_exposure possible\_cis effect\_allele\_outcome other\_allele\_outcome eaf\_outcome beta\_outcome se\_outcome

cd "//Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

file open table2 using "Regression MR results TIM-1 vs plaque.txt", replace write

file write table2 "Test" \_tab "Beta" \_tab "CIlow" \_tab "CIhigh" \_tab "P-value" \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //MR Egger med Q

file write table2 "MR Egger" \_tab (round(\_b[slope]),0.0001) \_tab (round(\_b[slope]-1.96\*\_se[slope]),0.0001) \_tab (round(\_b[slope]+1.96\*\_se[slope]),0.0001) \_tab (round(2\*(1-normal(abs(\_b[slope]/\_se[slope]))),0.0000000000001)) \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], ivw fe //IVW

file write table2 "IVW" \_tab (round(\_b[beta\_exposure]),0.0001) \_tab (round(\_b[beta\_exposure]-1.96\*\_se[beta\_exposure]),0.0001) \_tab (round(\_b[beta\_exposure]+1.96\*\_se[beta\_exposure]),0.001) \_tab (round(2\*(1-normal(abs(\_b[beta\_exposure]/\_se[beta\_exposure]))),0.0000000000001)) \_n

mrmedian beta\_outcome se\_outcome beta\_exposure se\_exposure, weighted // Weighted median

file write table2 "Weighted median" \_tab (round(\_b[beta]),0.0001) \_tab (round(\_b[beta]-1.96\*\_se[beta]),0.0001) \_tab (round(\_b[beta]+1.96\*\_se[beta]),0.001) \_tab (round(2\*(1-normal(abs(\_b[beta]/\_se[beta]))),0.0000000000001)) \_n

file write table2 "Heterogeneity" \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //MR Egger med Q

file write table2 "Pleiotropy" \_tab (round(\_b[\_cons]),0.0001) \_tab (round(\_b[\_cons]-1.96\*\_se[\_cons]),0.0001) \_tab (round(\_b[\_cons]+1.96\*\_se[\_cons]),0.001) \_tab (round(2\*(1-normal(abs(\_b[\_cons]/\_se[\_cons]))),0.0000000000001)) \_n

file close table2

mrivests beta\_outcome se\_outcome beta\_exposure se\_exposure, generate(ivest ivse) //genererar causal estimates och se, mregger funkar ej med 2 SNPs, behövs 3.

keep if rsid=="rs6555820" //rrs72981675

mrratio beta\_outcome se\_outcome beta\_exposure se\_exposure

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*. IL-6 (1 trans)

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/SCALLOP proteininstrument.dta"

keep if name=="IL-6"

drop n

sort rsid

merge rsid using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/GWAS results IMT.dta"

tab \_merge

drop if \_merge!=3 // (alla 6 kvar)

list rsid

keep rsid effect\_allele\_exposure other\_allele\_exposure eaf\_exposure beta\_exposure se\_exposure possible\_cis effect\_allele\_outcome other\_allele\_outcome eaf\_outcome beta\_outcome se\_outcome

\*imt

\*mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //konvergerar ej med 3 SNPs

mrivests beta\_outcome se\_outcome beta\_exposure se\_exposure, generate(ivest ivse) //genererar causal estimates och se, mregger funkar ej med 2 SNPs, behövs 3.

mrratio beta\_outcome se\_outcome beta\_exposure se\_exposure

\*plaque

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/SCALLOP proteininstrument.dta"

keep if name=="IL-6"

drop n

\*replace rsid="rs1050317" if rsid=="rs9264664" //byter ut mot proxy

sort rsid

merge rsid using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/GWAS results plaque.dta"

tab \_merge

drop if \_merge!=3 // (alla 4 kvar)

list rsid

keep rsid effect\_allele\_exposure other\_allele\_exposure eaf\_exposure beta\_exposure se\_exposure possible\_cis effect\_allele\_outcome other\_allele\_outcome eaf\_outcome beta\_outcome se\_outcome

\*mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //konvergerar ej med 3 SNPs

mrivests beta\_outcome se\_outcome beta\_exposure se\_exposure, generate(ivest ivse) //genererar causal estimates och se, mregger funkar ej med 2 SNPs, behövs 3.

mrratio beta\_outcome se\_outcome beta\_exposure se\_exposure

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*. U-PAR

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/SCALLOP proteininstrument.dta"

keep if name=="U-PAR"

drop n

sort rsid

merge rsid using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/GWAS results IMT.dta"

tab \_merge

drop if \_merge!=3 // (alla 6 kvar)

list rsid

keep rsid effect\_allele\_exposure other\_allele\_exposure eaf\_exposure beta\_exposure se\_exposure possible\_cis effect\_allele\_outcome other\_allele\_outcome eaf\_outcome beta\_outcome se\_outcome

\*imt

cd "//Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

file open table2 using "Regression MR results UPAR vs IMT.txt", replace write

file write table2 "Test" \_tab "Beta" \_tab "CIlow" \_tab "CIhigh" \_tab "P-value" \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //MR Egger med Q

file write table2 "MR Egger" \_tab (round(\_b[slope]),0.0001) \_tab (round(\_b[slope]-1.96\*\_se[slope]),0.0001) \_tab (round(\_b[slope]+1.96\*\_se[slope]),0.0001) \_tab (round(2\*(1-normal(abs(\_b[slope]/\_se[slope]))),0.0000000000001)) \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], ivw fe //IVW

file write table2 "IVW" \_tab (round(\_b[beta\_exposure]),0.0001) \_tab (round(\_b[beta\_exposure]-1.96\*\_se[beta\_exposure]),0.0001) \_tab (round(\_b[beta\_exposure]+1.96\*\_se[beta\_exposure]),0.001) \_tab (round(2\*(1-normal(abs(\_b[beta\_exposure]/\_se[beta\_exposure]))),0.0000000000001)) \_n

mrmedian beta\_outcome se\_outcome beta\_exposure se\_exposure, weighted // Weighted median

file write table2 "Weighted median" \_tab (round(\_b[beta]),0.0001) \_tab (round(\_b[beta]-1.96\*\_se[beta]),0.0001) \_tab (round(\_b[beta]+1.96\*\_se[beta]),0.001) \_tab (round(2\*(1-normal(abs(\_b[beta]/\_se[beta]))),0.0000000000001)) \_n

file write table2 "Heterogeneity" \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //MR Egger med Q

file write table2 "Pleiotropy" \_tab (round(\_b[\_cons]),0.0001) \_tab (round(\_b[\_cons]-1.96\*\_se[\_cons]),0.0001) \_tab (round(\_b[\_cons]+1.96\*\_se[\_cons]),0.001) \_tab (round(2\*(1-normal(abs(\_b[\_cons]/\_se[\_cons]))),0.0000000000001)) \_n

file close table2

mrivests beta\_outcome se\_outcome beta\_exposure se\_exposure, generate(ivest ivse) //genererar causal estimates och se, mregger funkar ej med 2 SNPs, behövs 3.

keep if rsid=="rs2302524" //rrs72981675

mrratio beta\_outcome se\_outcome beta\_exposure se\_exposure

\*plaque

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/SCALLOP proteininstrument.dta"

keep if name=="U-PAR"

drop n

\*replace rsid="rs1050317" if rsid=="rs9264664" //byter ut mot proxy

sort rsid

merge rsid using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/GWAS results plaque.dta"

tab \_merge

drop if \_merge!=3 // (alla 4 kvar)

list rsid

keep rsid effect\_allele\_exposure other\_allele\_exposure eaf\_exposure beta\_exposure se\_exposure possible\_cis effect\_allele\_outcome other\_allele\_outcome eaf\_outcome beta\_outcome se\_outcome

cd "//Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

file open table2 using "Regression MR results UPAR vs plaque.txt", replace write

file write table2 "Test" \_tab "Beta" \_tab "CIlow" \_tab "CIhigh" \_tab "P-value" \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //MR Egger med Q

file write table2 "MR Egger" \_tab (round(\_b[slope]),0.0001) \_tab (round(\_b[slope]-1.96\*\_se[slope]),0.0001) \_tab (round(\_b[slope]+1.96\*\_se[slope]),0.0001) \_tab (round(2\*(1-normal(abs(\_b[slope]/\_se[slope]))),0.0000000000001)) \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], ivw fe //IVW

file write table2 "IVW" \_tab (round(\_b[beta\_exposure]),0.0001) \_tab (round(\_b[beta\_exposure]-1.96\*\_se[beta\_exposure]),0.0001) \_tab (round(\_b[beta\_exposure]+1.96\*\_se[beta\_exposure]),0.001) \_tab (round(2\*(1-normal(abs(\_b[beta\_exposure]/\_se[beta\_exposure]))),0.0000000000001)) \_n

mrmedian beta\_outcome se\_outcome beta\_exposure se\_exposure, weighted // Weighted median

file write table2 "Weighted median" \_tab (round(\_b[beta]),0.0001) \_tab (round(\_b[beta]-1.96\*\_se[beta]),0.0001) \_tab (round(\_b[beta]+1.96\*\_se[beta]),0.001) \_tab (round(2\*(1-normal(abs(\_b[beta]/\_se[beta]))),0.0000000000001)) \_n

file write table2 "Heterogeneity" \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //MR Egger med Q

file write table2 "Pleiotropy" \_tab (round(\_b[\_cons]),0.0001) \_tab (round(\_b[\_cons]-1.96\*\_se[\_cons]),0.0001) \_tab (round(\_b[\_cons]+1.96\*\_se[\_cons]),0.001) \_tab (round(2\*(1-normal(abs(\_b[\_cons]/\_se[\_cons]))),0.0000000000001)) \_n

file close table2

mrivests beta\_outcome se\_outcome beta\_exposure se\_exposure, generate(ivest ivse) //genererar causal estimates och se, mregger funkar ej med 2 SNPs, behövs 3.

keep if rsid=="rs2302524" //rrs72981675

mrratio beta\_outcome se\_outcome beta\_exposure se\_exposure

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*. TRAIL-R2 (2 cis)

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/SCALLOP proteininstrument.dta"

keep if name=="TRAIL-R2"

drop n

sort rsid

merge rsid using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/GWAS results IMT.dta"

tab \_merge

drop if \_merge!=3 // (alla 6 kvar)

list rsid

keep rsid effect\_allele\_exposure other\_allele\_exposure eaf\_exposure beta\_exposure se\_exposure possible\_cis effect\_allele\_outcome other\_allele\_outcome eaf\_outcome beta\_outcome se\_outcome

\*imt

\*mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //konvergerar ej med 3 SNPs

mrivests beta\_outcome se\_outcome beta\_exposure se\_exposure, generate(ivest ivse) //genererar causal estimates och se, mregger funkar ej med 2 SNPs, behövs 3.

metan ivest ivse, fixed nograph

metan ivest ivse if rsid!="rs79287178", fixed nograph

keep if rsid=="rs2293400" //rs148339496

mrratio beta\_outcome se\_outcome beta\_exposure se\_exposure

\*plaque

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/SCALLOP proteininstrument.dta"

keep if name=="TRAIL-R2"

drop n

\*replace rsid="rs1050317" if rsid=="rs9264664" //byter ut mot proxy

sort rsid

merge rsid using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/GWAS results plaque.dta"

tab \_merge

drop if \_merge!=3 // (alla 4 kvar)

list rsid

keep rsid effect\_allele\_exposure other\_allele\_exposure eaf\_exposure beta\_exposure se\_exposure possible\_cis effect\_allele\_outcome other\_allele\_outcome eaf\_outcome beta\_outcome se\_outcome

\*mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //konvergerar ej med 3 SNPs

mrivests beta\_outcome se\_outcome beta\_exposure se\_exposure, generate(ivest ivse) //genererar causal estimates och se, mregger funkar ej med 2 SNPs, behövs 3.

metan ivest ivse, fixed nograph

metan ivest ivse if rsid!="rs79287178", fixed nograph

keep if rsid=="rs2293400" //rs148339496

mrratio beta\_outcome se\_outcome beta\_exposure se\_exposure

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* LOX-1 (5 SNPs varav 1 cis)

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/SCALLOP proteininstrument.dta"

keep if name=="LOX-1"

drop n

sort rsid

merge rsid using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/GWAS results IMT.dta"

tab \_merge

drop if \_merge!=3 // (alla 6 kvar)

list rsid

keep rsid effect\_allele\_exposure other\_allele\_exposure eaf\_exposure beta\_exposure se\_exposure possible\_cis effect\_allele\_outcome other\_allele\_outcome eaf\_outcome beta\_outcome se\_outcome

drop if rsid=="rs138226373"

\*imt

cd "//Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

file open table2 using "Regression MR results LOX1 vs IMT.txt", replace write

file write table2 "Test" \_tab "Beta" \_tab "CIlow" \_tab "CIhigh" \_tab "P-value" \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //MR Egger med Q

file write table2 "MR Egger" \_tab (round(\_b[slope]),0.0001) \_tab (round(\_b[slope]-1.96\*\_se[slope]),0.0001) \_tab (round(\_b[slope]+1.96\*\_se[slope]),0.0001) \_tab (round(2\*(1-normal(abs(\_b[slope]/\_se[slope]))),0.0000000000001)) \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], ivw fe //IVW

file write table2 "IVW" \_tab (round(\_b[beta\_exposure]),0.0001) \_tab (round(\_b[beta\_exposure]-1.96\*\_se[beta\_exposure]),0.0001) \_tab (round(\_b[beta\_exposure]+1.96\*\_se[beta\_exposure]),0.001) \_tab (round(2\*(1-normal(abs(\_b[beta\_exposure]/\_se[beta\_exposure]))),0.0000000000001)) \_n

mrmedian beta\_outcome se\_outcome beta\_exposure se\_exposure, weighted // Weighted median

file write table2 "Weighted median" \_tab (round(\_b[beta]),0.0001) \_tab (round(\_b[beta]-1.96\*\_se[beta]),0.0001) \_tab (round(\_b[beta]+1.96\*\_se[beta]),0.001) \_tab (round(2\*(1-normal(abs(\_b[beta]/\_se[beta]))),0.0000000000001)) \_n

file write table2 "Heterogeneity" \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //MR Egger med Q

file write table2 "Pleiotropy" \_tab (round(\_b[\_cons]),0.0001) \_tab (round(\_b[\_cons]-1.96\*\_se[\_cons]),0.0001) \_tab (round(\_b[\_cons]+1.96\*\_se[\_cons]),0.001) \_tab (round(2\*(1-normal(abs(\_b[\_cons]/\_se[\_cons]))),0.0000000000001)) \_n

file close table2

mrivests beta\_outcome se\_outcome beta\_exposure se\_exposure, generate(ivest ivse) //genererar causal estimates och se, mregger funkar ej med 2 SNPs, behövs 3.

keep if rsid=="rs10505752" //rrs72981675

mrratio beta\_outcome se\_outcome beta\_exposure se\_exposure

\*plaque

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/SCALLOP proteininstrument.dta"

keep if name=="LOX-1"

drop n

\*replace rsid="rs1050317" if rsid=="rs9264664" //byter ut mot proxy

sort rsid

merge rsid using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/GWAS results plaque.dta"

tab \_merge

drop if \_merge!=3 // (alla 4 kvar)

list rsid

keep rsid effect\_allele\_exposure other\_allele\_exposure eaf\_exposure beta\_exposure se\_exposure possible\_cis effect\_allele\_outcome other\_allele\_outcome eaf\_outcome beta\_outcome se\_outcome

drop if rsid=="rs138226373"

cd "//Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

file open table2 using "Regression MR results LOX1 vs plaque.txt", replace write

file write table2 "Test" \_tab "Beta" \_tab "CIlow" \_tab "CIhigh" \_tab "P-value" \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //MR Egger med Q

file write table2 "MR Egger" \_tab (round(\_b[slope]),0.0001) \_tab (round(\_b[slope]-1.96\*\_se[slope]),0.0001) \_tab (round(\_b[slope]+1.96\*\_se[slope]),0.0001) \_tab (round(2\*(1-normal(abs(\_b[slope]/\_se[slope]))),0.0000000000001)) \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], ivw fe //IVW

file write table2 "IVW" \_tab (round(\_b[beta\_exposure]),0.0001) \_tab (round(\_b[beta\_exposure]-1.96\*\_se[beta\_exposure]),0.0001) \_tab (round(\_b[beta\_exposure]+1.96\*\_se[beta\_exposure]),0.001) \_tab (round(2\*(1-normal(abs(\_b[beta\_exposure]/\_se[beta\_exposure]))),0.0000000000001)) \_n

mrmedian beta\_outcome se\_outcome beta\_exposure se\_exposure, weighted // Weighted median

file write table2 "Weighted median" \_tab (round(\_b[beta]),0.0001) \_tab (round(\_b[beta]-1.96\*\_se[beta]),0.0001) \_tab (round(\_b[beta]+1.96\*\_se[beta]),0.001) \_tab (round(2\*(1-normal(abs(\_b[beta]/\_se[beta]))),0.0000000000001)) \_n

file write table2 "Heterogeneity" \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //MR Egger med Q

file write table2 "Pleiotropy" \_tab (round(\_b[\_cons]),0.0001) \_tab (round(\_b[\_cons]-1.96\*\_se[\_cons]),0.0001) \_tab (round(\_b[\_cons]+1.96\*\_se[\_cons]),0.001) \_tab (round(2\*(1-normal(abs(\_b[\_cons]/\_se[\_cons]))),0.0000000000001)) \_n

file close table2

mrivests beta\_outcome se\_outcome beta\_exposure se\_exposure, generate(ivest ivse) //genererar causal estimates och se, mregger funkar ej med 2 SNPs, behövs 3.

keep if rsid=="rs10505752" //rrs72981675

mrratio beta\_outcome se\_outcome beta\_exposure se\_exposure

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*. MMP-10 ( 3 st varav 2 cis)

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/SCALLOP proteininstrument.dta"

keep if name=="MMP-10"

drop n

sort rsid

merge rsid using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/GWAS results IMT.dta"

tab \_merge

drop if \_merge!=3 // (alla 6 kvar)

list rsid

keep rsid effect\_allele\_exposure other\_allele\_exposure eaf\_exposure beta\_exposure se\_exposure possible\_cis effect\_allele\_outcome other\_allele\_outcome eaf\_outcome beta\_outcome se\_outcome

\*imt

\*mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //konvergerar ej med 3 SNPs

mrivests beta\_outcome se\_outcome beta\_exposure se\_exposure, generate(ivest ivse) //genererar causal estimates och se, mregger funkar ej med 2 SNPs, behövs 3.

metan ivest ivse, fixed nograph

metan ivest ivse if rsid!="rs601338", fixed nograph

metan ivest ivse if rsid=="rs17860955", fixed nograph

metan ivest ivse if rsid=="rs2012390", fixed nograph

\*plaque

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/SCALLOP proteininstrument.dta"

keep if name=="MMP-10"

drop n

\*replace rsid="rs1050317" if rsid=="rs9264664" //byter ut mot proxy

sort rsid

merge rsid using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/GWAS results plaque.dta"

tab \_merge

drop if \_merge!=3 // (alla 4 kvar)

list rsid

keep rsid effect\_allele\_exposure other\_allele\_exposure eaf\_exposure beta\_exposure se\_exposure possible\_cis effect\_allele\_outcome other\_allele\_outcome eaf\_outcome beta\_outcome se\_outcome

mrivests beta\_outcome se\_outcome beta\_exposure se\_exposure, generate(ivest ivse) //genererar causal estimates och se, mregger funkar ej med 2 SNPs, behövs 3.

metan ivest ivse, fixed nograph

metan ivest ivse if rsid!="rs601338", fixed nograph

metan ivest ivse if rsid=="rs17860955", fixed nograph

metan ivest ivse if rsid=="rs2012390", fixed nograph

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* LEP

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/SCALLOP proteininstrument.dta"

keep if name=="LEP"

drop n

sort rsid

merge rsid using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/GWAS results IMT.dta"

tab \_merge

drop if \_merge!=3 // (alla 6 kvar)

list rsid

keep rsid effect\_allele\_exposure other\_allele\_exposure eaf\_exposure beta\_exposure se\_exposure possible\_cis effect\_allele\_outcome other\_allele\_outcome eaf\_outcome beta\_outcome se\_outcome

\*imt

\*mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //konvergerar ej med 3 SNPs

mrivests beta\_outcome se\_outcome beta\_exposure se\_exposure, generate(ivest ivse) //genererar causal estimates och se, mregger funkar ej med 2 SNPs, behövs 3.

metan ivest ivse, fixed nograph

metan ivest ivse if rsid=="rs12537573", fixed nograph

\*plaque

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/SCALLOP proteininstrument.dta"

keep if name=="LEP"

drop n

\*replace rsid="rs1050317" if rsid=="rs9264664" //byter ut mot proxy

sort rsid

merge rsid using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/GWAS results plaque.dta"

tab \_merge

drop if \_merge!=3 // (alla 4 kvar)

list rsid

keep rsid effect\_allele\_exposure other\_allele\_exposure eaf\_exposure beta\_exposure se\_exposure possible\_cis effect\_allele\_outcome other\_allele\_outcome eaf\_outcome beta\_outcome se\_outcome

mrivests beta\_outcome se\_outcome beta\_exposure se\_exposure, generate(ivest ivse) //genererar causal estimates och se, mregger funkar ej med 2 SNPs, behövs 3.

metan ivest ivse, fixed nograph

metan ivest ivse if rsid=="rs12537573", fixed nograph

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*ADM (4 st, 1 cis)

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/SCALLOP proteininstrument.dta"

keep if name=="ADM"

drop n

replace rsid="rs1050317" if rsid=="rs9264664" //byter ut mot proxy

sort rsid

merge rsid using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/GWAS results IMT.dta"

tab \_merge

drop if \_merge!=3 // (3 kvar) missar rs9264664

list rsid

keep rsid effect\_allele\_exposure other\_allele\_exposure eaf\_exposure beta\_exposure se\_exposure possible\_cis effect\_allele\_outcome other\_allele\_outcome eaf\_outcome beta\_outcome se\_outcome

\*imt

cd "//Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

file open table2 using "Regression MR results ADM vs IMT.txt", replace write

file write table2 "Test" \_tab "Beta" \_tab "CIlow" \_tab "CIhigh" \_tab "P-value" \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //MR Egger med Q

file write table2 "MR Egger" \_tab (round(\_b[slope]),0.0001) \_tab (round(\_b[slope]-1.96\*\_se[slope]),0.0001) \_tab (round(\_b[slope]+1.96\*\_se[slope]),0.0001) \_tab (round(2\*(1-normal(abs(\_b[slope]/\_se[slope]))),0.0000000000001)) \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], ivw fe //IVW

file write table2 "IVW" \_tab (round(\_b[beta\_exposure]),0.0001) \_tab (round(\_b[beta\_exposure]-1.96\*\_se[beta\_exposure]),0.0001) \_tab (round(\_b[beta\_exposure]+1.96\*\_se[beta\_exposure]),0.001) \_tab (round(2\*(1-normal(abs(\_b[beta\_exposure]/\_se[beta\_exposure]))),0.0000000000001)) \_n

mrmedian beta\_outcome se\_outcome beta\_exposure se\_exposure, weighted // Weighted median

file write table2 "Weighted median" \_tab (round(\_b[beta]),0.0001) \_tab (round(\_b[beta]-1.96\*\_se[beta]),0.0001) \_tab (round(\_b[beta]+1.96\*\_se[beta]),0.001) \_tab (round(2\*(1-normal(abs(\_b[beta]/\_se[beta]))),0.0000000000001)) \_n

file write table2 "Heterogeneity" \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //MR Egger med Q

file write table2 "Pleiotropy" \_tab (round(\_b[\_cons]),0.0001) \_tab (round(\_b[\_cons]-1.96\*\_se[\_cons]),0.0001) \_tab (round(\_b[\_cons]+1.96\*\_se[\_cons]),0.001) \_tab (round(2\*(1-normal(abs(\_b[\_cons]/\_se[\_cons]))),0.0000000000001)) \_n

file close table2

mrivests beta\_outcome se\_outcome beta\_exposure se\_exposure, generate(ivest ivse) //genererar causal estimates och se, mregger funkar ej med 2 SNPs, behövs 3.

metan ivest ivse, fixed nograph

Study | ES [95% Conf. Interval] % Weight

---------------------+---------------------------------------------------

1 | -0.007 -0.030 0.016 10.96

2 | -0.003 -0.013 0.008 54.96

3 | 0.006 -0.007 0.018 34.08

---------------------+---------------------------------------------------

I-V pooled ES | -0.000 -0.008 0.007 100.00

---------------------+---------------------------------------------------

Heterogeneity chi-squared = 1.33 (d.f. = 2) p = 0.514

I-squared (variation in ES attributable to heterogeneity) = 0.0%

Test of ES=0 : z= 0.07 p = 0.944

keep if possible\_cis=="Y" //rs148339496

mrratio beta\_outcome se\_outcome beta\_exposure se\_exposure

------------------------------------------------------------------------------

| Coef. Std. Err. z P>|z| [95% Conf. Interval]

-------------+----------------------------------------------------------------

beta | -.002579 .0051614 -0.50 0.617 -.0126951 .0075371

------------------------------------------------------------------------------

\*plaque

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/SCALLOP proteininstrument.dta"

keep if name=="ADM"

drop n

replace rsid="rs1050317" if rsid=="rs9264664" //byter ut mot proxy

sort rsid

merge rsid using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/GWAS results plaque.dta"

tab \_merge

drop if \_merge!=3 // (3 kvar) missar rs9264664

list rsid

keep rsid effect\_allele\_exposure other\_allele\_exposure eaf\_exposure beta\_exposure se\_exposure possible\_cis effect\_allele\_outcome other\_allele\_outcome eaf\_outcome beta\_outcome se\_outcome

\*imt

cd "//Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

file open table2 using "Regression MR results ADM vs plaque.txt", replace write

file write table2 "Test" \_tab "Beta" \_tab "CIlow" \_tab "CIhigh" \_tab "P-value" \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //MR Egger med Q

file write table2 "MR Egger" \_tab (round(\_b[slope]),0.0001) \_tab (round(\_b[slope]-1.96\*\_se[slope]),0.0001) \_tab (round(\_b[slope]+1.96\*\_se[slope]),0.0001) \_tab (round(2\*(1-normal(abs(\_b[slope]/\_se[slope]))),0.0000000000001)) \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], ivw fe //IVW

file write table2 "IVW" \_tab (round(\_b[beta\_exposure]),0.0001) \_tab (round(\_b[beta\_exposure]-1.96\*\_se[beta\_exposure]),0.0001) \_tab (round(\_b[beta\_exposure]+1.96\*\_se[beta\_exposure]),0.001) \_tab (round(2\*(1-normal(abs(\_b[beta\_exposure]/\_se[beta\_exposure]))),0.0000000000001)) \_n

mrmedian beta\_outcome se\_outcome beta\_exposure se\_exposure, weighted // Weighted median

file write table2 "Weighted median" \_tab (round(\_b[beta]),0.0001) \_tab (round(\_b[beta]-1.96\*\_se[beta]),0.0001) \_tab (round(\_b[beta]+1.96\*\_se[beta]),0.001) \_tab (round(2\*(1-normal(abs(\_b[beta]/\_se[beta]))),0.0000000000001)) \_n

file write table2 "Heterogeneity" \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //MR Egger med Q

file write table2 "Pleiotropy" \_tab (round(\_b[\_cons]),0.0001) \_tab (round(\_b[\_cons]-1.96\*\_se[\_cons]),0.0001) \_tab (round(\_b[\_cons]+1.96\*\_se[\_cons]),0.001) \_tab (round(2\*(1-normal(abs(\_b[\_cons]/\_se[\_cons]))),0.0000000000001)) \_n

file close table2

mrivests beta\_outcome se\_outcome beta\_exposure se\_exposure, generate(ivest ivse) //genererar causal estimates och se, mregger funkar ej med 2 SNPs, behövs 3.

keep if possible\_cis=="Y" //rs148339496

mrratio beta\_outcome se\_outcome beta\_exposure se\_exposure

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* AGRP (4 SNP, 1 cis)

\*imt

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/SCALLOP proteininstrument.dta"

keep if name=="AGRP"

drop n

\*replace rsid="rs1050317" if rsid=="rs9264664" //byter ut mot proxy

sort rsid

merge rsid using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/GWAS results IMT.dta"

tab \_merge

drop if \_merge!=3 // hittar bara 2 trans

list rsid

keep rsid effect\_allele\_exposure other\_allele\_exposure eaf\_exposure beta\_exposure se\_exposure possible\_cis effect\_allele\_outcome other\_allele\_outcome eaf\_outcome beta\_outcome se\_outcome

mrivests beta\_outcome se\_outcome beta\_exposure se\_exposure, generate(ivest ivse) //genererar causal estimates och se, mregger funkar ej med 2 SNPs, behövs 3.

metan ivest ivse, fixed nograph

\*plaque

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/SCALLOP proteininstrument.dta"

keep if name=="AGRP"

drop n

\*replace rsid="rs1050317" if rsid=="rs9264664" //byter ut mot proxy

sort rsid

merge rsid using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/GWAS results plaque.dta"

tab \_merge

drop if \_merge!=3 // hittar bara 2 trans

list rsid

keep rsid effect\_allele\_exposure other\_allele\_exposure eaf\_exposure beta\_exposure se\_exposure possible\_cis effect\_allele\_outcome other\_allele\_outcome eaf\_outcome beta\_outcome se\_outcome

mrivests beta\_outcome se\_outcome beta\_exposure se\_exposure, generate(ivest ivse) //genererar causal estimates och se, mregger funkar ej med 2 SNPs, behövs 3.

metan ivest ivse, fixed nograph

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* CA-125 (4 snps, 1 trans)

\*imt

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/SCALLOP proteininstrument.dta"

keep if name=="CA-125"

drop n

\*replace rsid="rs1050317" if rsid=="rs9264664" //byter ut mot proxy

sort rsid

merge rsid using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/GWAS results IMT.dta"

tab \_merge

drop if \_merge!=3 // hittar alla 4

list rsid

keep rsid effect\_allele\_exposure other\_allele\_exposure eaf\_exposure beta\_exposure se\_exposure possible\_cis effect\_allele\_outcome other\_allele\_outcome eaf\_outcome beta\_outcome se\_outcome

mrivests beta\_outcome se\_outcome beta\_exposure se\_exposure, generate(ivest ivse) //genererar causal estimates och se, mregger funkar ej med 2 SNPs, behövs 3.

metan ivest ivse, fixed nograph

mrivests beta\_outcome se\_outcome beta\_exposure se\_exposure, generate(ivest ivse) //genererar causal estimates och se, mregger funkar ej med 2 SNPs, behövs 3.

keep if possible\_cis=="Y" //rs11672713

mrratio beta\_outcome se\_outcome beta\_exposure se\_exposure

\*plaque

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/SCALLOP proteininstrument.dta"

keep if name=="CA-125"

drop n

\*replace rsid="rs1050317" if rsid=="rs9264664" //byter ut mot proxy

sort rsid

merge rsid using "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/GWAS results plaque.dta"

tab \_merge

drop if \_merge!=3 // hittar alla 4

list rsid

keep rsid effect\_allele\_exposure other\_allele\_exposure eaf\_exposure beta\_exposure se\_exposure possible\_cis effect\_allele\_outcome other\_allele\_outcome eaf\_outcome beta\_outcome se\_outcome

cd "//Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/"

file open table2 using "Regression MR results CA-125 vs plaque.txt", replace write

file write table2 "Test" \_tab "Beta" \_tab "CIlow" \_tab "CIhigh" \_tab "P-value" \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //MR Egger med Q

file write table2 "MR Egger" \_tab (round(\_b[slope]),0.0001) \_tab (round(\_b[slope]-1.96\*\_se[slope]),0.0001) \_tab (round(\_b[slope]+1.96\*\_se[slope]),0.0001) \_tab (round(2\*(1-normal(abs(\_b[slope]/\_se[slope]))),0.0000000000001)) \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], ivw fe //IVW

file write table2 "IVW" \_tab (round(\_b[beta\_exposure]),0.0001) \_tab (round(\_b[beta\_exposure]-1.96\*\_se[beta\_exposure]),0.0001) \_tab (round(\_b[beta\_exposure]+1.96\*\_se[beta\_exposure]),0.001) \_tab (round(2\*(1-normal(abs(\_b[beta\_exposure]/\_se[beta\_exposure]))),0.0000000000001)) \_n

mrmedian beta\_outcome se\_outcome beta\_exposure se\_exposure, weighted // Weighted median

file write table2 "Weighted median" \_tab (round(\_b[beta]),0.0001) \_tab (round(\_b[beta]-1.96\*\_se[beta]),0.0001) \_tab (round(\_b[beta]+1.96\*\_se[beta]),0.001) \_tab (round(2\*(1-normal(abs(\_b[beta]/\_se[beta]))),0.0000000000001)) \_n

file write table2 "Heterogeneity" \_n

mregger beta\_outcome beta\_exposure [aw=1/(se\_outcome^2)], gxse(se\_exposure) heterogi //MR Egger med Q

file write table2 "Pleiotropy" \_tab (round(\_b[\_cons]),0.0001) \_tab (round(\_b[\_cons]-1.96\*\_se[\_cons]),0.0001) \_tab (round(\_b[\_cons]+1.96\*\_se[\_cons]),0.001) \_tab (round(2\*(1-normal(abs(\_b[\_cons]/\_se[\_cons]))),0.0000000000001)) \_n

file close table2

mrivests beta\_outcome se\_outcome beta\_exposure se\_exposure, generate(ivest ivse) //genererar causal estimates och se, mregger funkar ej med 2 SNPs, behövs 3.

keep if possible\_cis=="Y" //rs11672713

mrratio beta\_outcome se\_outcome beta\_exposure se\_exposure

\*\*\*\*\*\*\*\*\* CTSD vs glucose

clear

use "/Users/larslind/Lind kopior/Mendelian randomization/Nedladdningar/Manning\_2012\_GLUCOSE.dta", clear

ren effect\_allele effect\_allele\_outcome

ren other\_allele other\_allele\_outcome

ren maf eaf\_outcome

ren maineffects beta\_outcome

ren mainse se\_outcome

ren mainp p\_outcome

keep SNP effect\_allele\_outcome other\_allele\_outcome eaf\_outcome beta\_outcome se\_outcome p\_outcome

order SNP effect\_allele\_outcome other\_allele\_outcome eaf\_outcome beta\_outcome se\_outcome p\_outcome

sort SNP

save "/Users/larslind/Lind kopior/Mendelian randomization/Nedladdningar/Manning\_2012\_GLUCOSE\_outcome.dta"

clear

use "/Users/larslind/Lind kopior/Proteomics/Athero meta-analysis/SCALLOP proteininstrument.dta"

keep if name=="CTSD"

keep if possible\_cis=="Y"

ren rsid SNP

ren pval p\_exposure

keep SNP effect\_allele\_exposure other\_allele\_exposure eaf\_exposure beta\_exposure se\_exposure p\_exposure

order SNP effect\_allele\_exposure other\_allele\_exposure eaf\_exposure beta\_exposure se\_exposure p\_exposure

sort SNP

merge SNP using "/Users/larslind/Lind kopior/Mendelian randomization/Nedladdningar/Manning\_2012\_GLUCOSE\_outcome.dta"

tab \_merge

drop if \_merge!=3

drop \_merge

replace allele1="A" if allele1=="a"

replace allele1="T" if allele1=="t"

replace allele1="G" if allele1=="g"

replace allele1="C" if allele1=="c"

replace allele2="A" if allele2=="a"

replace allele2="T" if allele2=="t"

replace allele2="G" if allele2=="g"

replace allele2="C" if allele2=="c"

ren allele1 effect\_allele\_outcome

ren allele2 other\_allele\_outcome

ren freq1 eaf\_outcome

ren effect beta\_outcome

ren stderr se\_outcome

ren refid rsid

sort rsid